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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:05:23 ; Search time 153 Seconds
(without alignments)
940.199 Million cell updates/sec

Title: US-09-813-718-10_COPY_71_471

Perfect score: 2116

Sequence: 1 SNHGPDATEABEDFVDPWTV.....VTDEIVKFWTPRKLSFDFQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	401	5	AAG79549 TrpRS T1
2	2116	100.0	415	4	AAB47617 Human sup
3	2116	100.0	415	5	AAE13493 Human sup
4	2116	100.0	415	5	AAG79548 His6-tag
5	2116	100.0	415	6	ABU72386 Human sup
6	2116	100.0	437	4	AAB47616 Human min
7	2116	100.0	437	5	AAE13492 Human min
8	2116	100.0	437	5	AAG79547 His6-tag
9	2116	100.0	437	6	ABU72385 Human min
10	2116	100.0	471	7	ADF76576 Novel hum
11	2116	100.0	471	7	ABU64298 Human try
12	2116	100.0	471	7	ADN39916 Cancer/an
13	2116	100.0	471	8	ADJ75318 Marker ge
14	2116	100.0	471	8	ADP12573 Protein e
15	2116	100.0	484	4	AAB47615 Human ful
16	2116	100.0	484	5	AAE13491 Human try
17	2116	100.0	484	5	AAG79546 Full leng
18	2116	100.0	484	6	ABU72384 Human ful
19	2101	99.3	471	7	ADE25762 Human pro
20	2101	99.3	471	7	ADJ69429 Human hea
21	2101	99.3	471	8	ADE76998 Human pro
22	2101	99.3	471	8	ADQ30575 Pancreas
23	2101	99.3	475	3	AAB58220 Lung canc
24	2096	99.1	471	2	AAY05372 Human HCM
25	1988	94.0	378	5	AAG79541 TrpRS T2

ALIGNMENTS

RESULT 1

AAG79549

ID AAG79549 standard; protein; 401 AA.

XX AAG79549;

XX

DT 10-DEC-2002 (first entry)

XX

DE TrpRS T1 polypeptide.

XX

XX T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;

KW neovascular eye disease; age-related macular degeneration;

KW ocular complication; diabetes; rubecotic glaucoma; retinopathy;

KW prematurity; keratitis; ischaemic retinopathy; sickle cell;

KW pathological myopic; ocular histoplasmosis; pterygia; T1;

KW punitate innerchoroidopathy; retinal degeneration; growth factor;

KW vascularisation; vascular endothelial cell function; angiogenesis.

XX Homo sapiens.

OS

XX WO200267970-A1.

PN

XX 06-SEP-2002.

PD

XX 22-FEB-2002; 2002WO-US005185.

XX

PR 23-FEB-2001; 2001US-0270951P.

XX

PA (SCRI) SCRIPPS RES INST.

XX Schimmel P, Wakasugi K, Friedlander M;

XX WPI; 2002-698635/75.

XX

PT New polypeptides derived from human tryptophanyl-tRNA synthase, useful

for inhibiting ocular neovascularization in a patient, or for treating

neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis,

or pterygia.

XX

PS Example 1; Page 78-79; 83pp; English.

XX

CC This sequence represents a novel cleavage product, T1, of recombinant

human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2,

is water soluble and comprises residues 94-471 of full length TrpRS. The

water-soluble T2 polypeptide is useful for inhibiting ocular

neovascularisation in a patient. The T2 polypeptide is useful for

treating neovascular eye diseases, e.g. age-related macular degeneration,

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

ocular complications of diabetes, rubecotic glaucoma, retinopathy of

CC	prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),
CC	pathological myopic, ocular histoplasmosis, pterygia, or punitate
CC	innerschoidopathy. This polypeptide is particularly useful for treating
CC	retinal degeneration to prevent the damaging effects of trophic and
CC	growth factors, and for promoting vascularisation to retard retinal
CC	degeneration by enhancing blood flow to cells. These are also useful for
CC	regulating vascular endothelial cell function, and in particular, for
CC	inhibiting angiogenesis
XX	
SQ	Sequence 401 AA;
	Query Match 100.0%; Score 2116; DB 5; Length 401;
	Best Local Similarity 100.0%; Pred. NO. 1.6e-209; Indels 0; Gaps 0;
	Matches 401; Conservative 0; Mismatches 0;
QY	1 SNHGPDATAEEDFVDPTWOTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP
DB	1 SNHGPDATAEEDFVDPTWOTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP
QY	61 FLRGIFFSHRDMNQVLDAENKPPFYLTYGRGSSSEAMHVGHILPFIPTKWLQDVNP
DB	61 FLRGIFFSHRDMNQVLDAENKPPFYLTYGRGSSSEAMHVGHILPFIPTKWLQDVNP
QY	121 LVIQMTDDEKYLWKDLTLDAQAYDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN
DB	121 LVIQMTDDEKYLWKDLTLDAQAYDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN
QY	181 VVKIQHVTFNQVKGIFGFTSDSCIGKISFPAIQAPSFNSFPQIFDRDTIQCLIFCA
DB	181 VVKIQHVTFNQVKGIFGFTSDSCIGKISFPAIQAPSFNSFPQIFDRDTIQCLIFCA
QY	241 IDQDPYFRMTDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPSNFIPLDTAKQIKT
DB	241 IDQDPYFRMTDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPSNFIPLDTAKQIKT
QY	301 KVNKHFSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL
DB	301 KVNKHFSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL
QY	361 KKALIEVLQPLIAEHOARKEVTDEIVKEFMTPRKLSFDFQ 401
DB	361 KKALIEVLQPLIAEHOARKEVTDEIVKEFMTPRKLSFDFQ 401
RESULT 2	
AA047617	AA047617 standard; protein; 415 AA.
XX	AA047617;
XX	07-JAN-2002 (first entry)
XX	Human supermini Trprs.
XX	Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain;
XX	vascular endothelial cell function; burn; plastic surgery; abdomen;
XX	polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
XX	angiogenesis; graft; myocardial infarction; solid tumour; wound healing;
XX	dermal ulcer; diabetic ulcer; endothelialization;
XX	cryptophanyl-cRNA synthetase; trprs; vascular graft surgery.
OS	Homo sapiens.
XX	WO200174841-A1.
XX	11-OCT-2001.
XX	21-MAR-2001; 2001WO-US008966.
XX	31-MAR-2000; 2000US-0193471P.
XX	(SCRI) SCRIPPS RES INST.
XX	

DE Human supermini tryptophanyl t-RNA synthetase in pET20B.

XX Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase;
 KW TrpRS; vascular endothelial cell function; angiogenesis; wound healing;
 KW re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;
 KW diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;
 KW angiography; gene therapy; tumour; inflammation; vascular permeability;
 KW rheumatoid arthritis; psoriasis; diabetic retinopathy.

XX Homo sapiens.

XX W0200175078-A1.

XX 11-OCT-2001.

XX 21-MAR-2001; 2001WO-US008975.

XX 31-MAR-2000; 2000US-0193471P.

XX (SCRI) SCRIPPS RES INST.

XX Schimmel P, Wakasugi K;

XX WPI; 2002-010784/01.

XX N-PSDB; AAD22484.

XX Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of
 PT regulating vascular endothelial cell function, preferably angiogenesis,
 PT is useful for treating solid tumor or suppressing tumor metastasis in
 PT mammal.

XX Example 1; Page 129-130; 149pp; English.

XX The patent discloses human aminoacyl tRNA synthetases, particularly
 CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann
 CC fold nucleotide binding domain and polynucleotides encoding them. The
 CC invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS
 CC sequences are useful for regulating vascular endothelial cell function,
 CC preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound
 CC healing agents for re-vascularising damaged tissues. They are useful for
 CC treating full-thickness wounds (e.g. dermal ulcers, including pressure
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS
 CC sequences can also be used in plastic surgery when reconstruction is
 CC required following a burn, other trauma, or even for cosmetic purposes.
 CC Angiogenic TrpRS is also used in association with surgery and following
 CC the repair of cuts, for promoting endothelialisation in vascular graft
 CC surgery and for repairing the damage of myocardial infarction and in
 CC conjunction with coronary bypass surgery by stimulating the growth of
 CC transplanted tissue. TrpRS is also used in conjunction with angiography.
 CC TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in
 CC immunoassays to detect the presence of tumours. They are also useful for
 CC blocking endogenous angiogenic activity and retard the growth of solid
 CC tumours. These antibodies may also be used to treat inflammation caused
 CC by increased vascular permeability. Inhibiting the activity of TrpRS by
 CC antisense technology is useful for preventing further growth or even
 CC regress solid tumours, and for treating rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, all of which are characterised by abnormal
 CC angiogenesis. The present sequence is human truncated tryptophanyl t-RNA
 CC synthetase (supermini TrpRS; residues 71-471 of full-length TrpRS
 CC protein) in pET20B

XX Query Match 100.0%; Score 2116; DB 5; Length 415;
 XX Best Local Similarity 100.0%; Pred. No. 1.7e-209;
 XX Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTOTSSAKGIDYDKLIVRFSSKIDKELINRIERATGQRPHH 60
 Db 2 SNHGPDTEAEEDFVDPWTOTSSAKGIDYDKLIVRFSSKIDKELINRIERATGQRPHH 61
 Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGPSSSEAMVGHILPIFTKWLQDVFNVP 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 62 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGPSSSEAMVGHILPIFTKWLQDVFNVP 121
 Qy 121 LVQIMTDDEKYLKWLDTLDQAYGDAVENAKDIIACGPDINKTIFISDLDMGMSGGFYKN 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 122 LVQIMTDDEKYLKWLDTLDQAYGDAVENAKDIIACGPDINKTIFISDLDMGMSGGFYKN 181
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 181 VVKIQHVTNQVKGIFGFTDSDICIGKISPPAQAPSFNSPPOIFRDRDTDIQCLIPCA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 182 VVKIQHVTNQVKGIFGFTDSDICIGKISPPAQAPSFNSPPOIFRDRDTDIQCLIPCA 241
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTQKMSADPNSSIFLDTAKQIKT 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTQKMSADPNSSIFLDTAKQIKT 301
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 301 KVAKHAFSGGRDTIEHRQFGNCDVDVSFMYLTFPLEDDDKLEIQIRKDYTSGLMTGEL 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 302 KVAKHAFSGGRDTIEHRQFGNCDVDVSFMYLTFPLEDDDKLEIQIRKDYTSGLMTGEL 361
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 401
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 402
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 4
 AAG79548
 ID AAG79548 standard; protein; 415 AA.
 XX
 AC AAG79548;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE DE
 XX
 XX His6-tagged TrpRS T1 polypeptide.
 KW T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;
 KW neovascular eye disease; age-related macular degeneration;
 KW ocular complication; diabetes; rubecotic glaucoma; retinopathy;
 KW prematurity; keratitis; ischaemic retinopathy; sickle cell;
 KW pathological myopic; ocular histoplasmosis; pterygia; T1;
 KW punitate innerchoroidopathy; retinal degeneration; growth factor;
 KW vascularisation; vascular endothelial cell function; angiogenesis.
 XX Homo sapiens.
 OS
 XX W0200267970-A1.
 FN
 XX
 XX 06-SEP-2002.
 PD
 XX
 XX 22-FEB-2002; 2002WO-US005185.
 PF
 XX
 XX 23-FEB-2001; 2001US-0270951P.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Schimmel P, Wakasugi K, Friedlander M;
 FI
 XX
 XX WPI; 2002-698635/75.
 DR
 XX
 XX N-PSDB; ABA00330.
 DR
 XX
 XX New polypeptides derived from human tryptophanyl-tRNA synthase, useful
 PT for inhibiting ocular neovascularization in a patient, or for treating
 PT neovascular eye diseases, e.g. rubecotic glaucoma, retinopathy, keratitis,
 PT or pterygia.
 PT
 XX
 XX Example 1; Page 71-72; 83pp; English.
 PS
 XX
 XX This sequence represents a His6-tagged cleavage product, T1, of
 CC recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage
 CC product, T2, is water soluble and comprises residues 94-471 of full
 CC length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting
 CC ocular neovascularisation in a patient. The T2 polypeptide is useful for
 CC treating neovascular eye diseases, e.g. age-related macular degeneration,
 CC ocular complications of diabetes, rubecotic glaucoma, retinopathy of
 CC prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),

CC pathological myopic, ocular histoplasmosis, pterygia, or punitate
 CC innerchoroidopathy. This polypeptide is particularly useful for treating
 CC retinal degeneration to prevent the damaging effects of trophic and
 CC growth factors, and for promoting vascularisation to retard retinal
 CC degeneration by enhancing blood flow to cells. These are also useful for
 CC regulating vascular endothelial cell function, and in particular, for
 CC inhibiting angiogenesis
 XX
 XX SQ Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 5; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.7e-209;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60
 Db 2 SNHGPDTEAEEDFVDPWTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 61
 Qy 61 FLRRGIFFSHRDMNQVLDAYENKPPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 120
 Db 62 FLRRGIFFSHRDMNQVLDAYENKPPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 121
 Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
 Db 122 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 181
 Qy 181 VVKIQKHVTNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFDRDRTDIOCLIPCA 240
 Db 182 VVKIQKHVTNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFDRDRTDIOCLIPCA 241
 Qy 241 IDQDPYFRMTDVA PRIGYPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 300
 Db 242 IDQDPYFRMTDVA PRIGYPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 301
 Qy 301 KVNKHAFIGSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360
 Db 302 KVNKHAFIGSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 361

RESULT 5

ID ABU72386
 XX ABU72386 standard; protein; 415 AA.

AC ABU72386;

DT 16-JUN-2003 (first entry)

DE Human supermini Tryptophanyl tRNA synthetase/His tag.

XX Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic;
 KW vulnery; Rossmann fold nucleotide binding domain; chemokine; EMAP II;
 KW vascular endothelial cell; solid tumour; myocardial infarction; enzyme;
 KW endothelial monocyte-activating polypeptide II; tumour metastasis;
 KW wound healing; dermal ulcer; endothelialisation; vascular graft surgery;
 KW abdominal wound; coronary bypass surgery; gene therapy.

XX Homo sapiens.

OS Synthetic.

PN US2002182666-A1.

XX 05-DEC-2002.

XX 21-MAR-2001; 2001US-00813718.

XX 21-MAR-2001; 2001US-00813718.

XX (SCHL/) SCHIMMEL P.

PA (WAKA/) WAKASUGI K.

Schimmel P, Wakasugi K;

WPI; 2003-340974/32.

N-PSDB; ACA64107.

New truncated tryptophanyl-tRNA synthetase polypeptide comprising a
 Rossmann fold nucleotide binding domain or having chemokine activity
 useful for e.g. for regulating angiogenesis and for treating myocardial
 infarction.

Example 1; Page 50-51; 9ipp; English.

The invention relates to an isolated polypeptide comprising a truncated
 tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann
 fold nucleotide binding domain or having chemokine activity. The isolated
 polypeptide is capable of regulating vascular endothelial cell function.
 TrpRS has a C-terminal domain containing an EMAP II (endothelial monocyte
 -activating polypeptide II, a proinflammatory cytokine)-like domain and
 is similar in sequence to TrpRS. Also included are a polynucleotide
 encoding TrpRS (or a polynucleotide 95% similar to it) a TrpRS epitope,
 5' and 3' deletions of the TrpRS polynucleotide, a recombinant vector
 comprising an isolated TrpRS nucleic acid, a recombinant host cell
 containing the TrpRS nucleic acid and expressing TrpRS, an isolated anti-
 TrpRS antibody, producing truncations of TrpRS by treating it with a
 protease, and suppressing angiogenesis, solid tumours or a condition that
 would benefit from decreased angiogenesis in a mammal by administering to
 the mammal the composition comprising the TrpRS truncated protein. The
 isolated polypeptide is useful for the preparation of a pharmaceutical
 composition for transdermal, transmucosal, enteral or parenteral
 administration. The truncated tRNA synthetase polypeptide is useful for
 research, diagnostic, prognostic and therapeutic applications. The tRNA
 synthetase are useful for regulating vascular endothelial cell function,
 particularly for regulating angiogenesis, for treating myocardial
 infarction and solid tumour, and for suppressing tumour metastasis.
 Angiogenic tRNA synthetase polypeptides are useful as wound healing
 agents or for treating full thickness wounds such as dermal ulcers, in
 the treatment of endothelialisation in vascular graft surgery, in the
 treatment of abdominal wounds where there is a high risk infection, in
 conjunction with coronary bypass surgery by stimulating the growth of the
 transplanted tissue, and in gene therapy. The present sequence is a Trp
 tRNA synthetase protein (full length, truncated or mutant) with a His
 affinity tag

Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 6; Length 415;

Best Local Similarity 100.0%; Pred. No. 1.7e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 2 SNHGPDTEAEEDFVDPWTVOTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 61

Qy 61 FLRRGIFFSHRDMNQVLDAYENKPPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 120

Db 62 FLRRGIFFSHRDMNQVLDAYENKPPFYLYTGRGSSSEAMVGHILPIFTKWLQDVNVP 121

Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180

Db 122 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 181

Qy 181 VVKIQKHVTNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFDRDRTDIOCLIPCA 240

Db 182 VVKIQKHVTNQVKGIFGFTSDCGIKISFPAIQAPSFNSFPQIFDRDRTDIOCLIPCA 241

Qy 241 IDQDPYFRMTDVA PRIGYPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 300

Db 242 IDQDPYFRMTDVA PRIGYPKALLHSTFFPALQAGQTKMSASDPNSIFLDTAKQIKT 301

Qy 301 KVNKHAFIGSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 302 KVNKHAFIGSGGRDTTIEHRQFGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 361

QY 361 KKALIEVLQPLIAHQARRKEVTDDEIVKEFWTPRKLSFDFQ 401
 ID AAB47616
 DB 362 KKALIEVLQPLIAHQARRKEVTDDEIVKEFWTPRKLSFDFQ 402

RESULT 6
 AAB47616
 ID AAB47616 standard; protein; 437 AA.
 AC AAB47616;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human mini TrpRS.
 XX
 KW Tyrosyl-tRNA synthetase; TrpRS; Rosemann fold nucleotide binding domain;
 KW vascular endothelial cell function; burn; plastic surgery; abdomen;
 KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
 KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;
 KW dermal ulcer; diabetic ulcer; endothelialization;
 KW tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
 XX
 OS Homo sapiens.
 XX
 PN WO200174841-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 21-MAR-2001; 2001WO-US008966.
 XX
 PR 31-MAR-2000; 2000US-0193471P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Schimmel P, Wakasugi K;
 XX
 DR WPI; 2001-626377/72.
 DR N-PSDB; AAH43603.
 XX
 PT New human truncated tyrosyl-tRNA synthetase polypeptide for regulating
 PT vascular endothelial function, in particular for regulating angiogenesis,
 PT tumor metastasis and treating myocardial infarction.
 XX
 PS Disclosure; Page 123-24; 150pp; English.
 XX
 CC The sequences given in AAB47615-18 show full length and truncated
 CC versions of tryptophanyl-tRNA synthetase (trpRS). The truncated trpRS of
 CC the invention comprises a Rosemann fold nucleotide binding domain, and is
 CC capable of regulating vascular endothelial cell function. It is of
 CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of
 CC full length TrpRS with polymorphonuclear leucocyte elastase. Truncated
 CC TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing
 CC angiogenesis to a graft, treating myocardial infarction, solid tumor, and
 CC a condition that would benefit from increased or decreased angiogenesis
 CC in a mammal, in particular humans. It is also useful in diagnosis and as
 CC a wound healing agent for treating wounds such as dermal ulcers, diabetic
 CC ulcers, burns and injuries and in plastic surgery when reconstruction is
 CC required following a burn or for cosmetic purposes. It is particularly
 CC useful in the treatment of abdominal wounds where there is high risk of
 CC infection. Truncated TrpRS promotes endothelialization in vascular graft
 CC surgery and is used in conjunction with angiography to administer the
 CC angiogenic tRNA synthetase polypeptides or polynucleotides directly to
 CC the lumen and wall of the blood vessel
 XX
 SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
 ID AAB47616
 DB 362 KKALIEVLQPLIAHQARRKEVTDDEIVKEFWTPRKLSFDFQ 402

RESULT 7
 AAE13492
 ID AAE13492 standard; protein; 437 AA.
 XX
 AC AAE13492;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Human mini tryptophanyl t-RNA synthetase in pET20B.
 XX
 KW Human; tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase;
 KW TrpRS; vascular endothelial cell function; angiogenesis; wound healing;
 KW re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;
 KW diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;
 KW angiography; gene therapy; tumour; inflammation; vascular permeability;
 KW rheumatoid arthritis; psoriasis; diabetic retinopathy.
 XX
 OS Homo sapiens.
 XX
 PN WO200175078-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 21-MAR-2001; 2001WO-US008975.
 XX
 PR 31-MAR-2000; 2000US-0193471P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Schimmel P, Wakasugi K;
 XX
 DR WPI; 2002-010784/01.
 DR N-PSDB; AAD22483.
 XX
 PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of
 PT regulating vascular endothelial cell function, preferably angiogenesis,
 PT is useful for treating solid tumor or suppressing tumor metastasis in
 PT mammal.
 XX
 PS Example 1; Page 123-124; 149pp; English.
 XX
 CC The patent discloses human aminoacyl tRNA synthetases, particularly
 CC truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rosemann
 CC fold nucleotide binding domain and polynucleotides encoding them. The
 CC invention also relates to tyrosyl t-RNA synthetases (TyRS). TrpRS
 CC sequences are useful for regulating vascular endothelial cell function,

CC preferably angiogenesis. Angiogenic TrpRS sequences are useful as wound
 CC healing agents for re-vascularising damaged tissues. They are useful for
 CC treating full-thickness wounds (e.g. dermal ulcers, including pressure
 CC sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS
 CC sequences can also be used in plastic surgery when reconstruction is
 CC required following a burn, other trauma, or even for cosmetic purposes.
 CC Angiogenic TrpRS is also used in association with surgery and following
 CC the repair of cuts, for promoting endothelialisation in vascular graft
 CC surgery and for repairing the damage of myocardial infarction and in
 CC conjunction with coronary bypass surgery by stimulating the growth of
 CC transplanted tissue. TrpRS is also used in conjunction with angiography.
 CC TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in
 CC immunoassays to detect the presence of tumours. They are also useful for
 CC blocking endogenous angiogenic activity and retard the growth of solid
 CC tumours. These antibodies may also be used to treat inflammation caused
 CC by increased vascular permeability. Inhibiting the activity of TrpRS by
 CC antisense technology is useful for preventing further growth or even
 CC regress solid tumours, and for treating rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, all of which are characterised by abnormal
 CC angiogenesis. The present sequence is human truncated tryptophanyl t-RNA
 CC synthetase (mini TrpRS; residues 48-471 of full-length TrpRS protein)
 CC protein in pET20B
 CC
 XX
 SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 5; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60
 DB 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 83
 QY 61 FLRRGIFPSHRDMNQVLDAVENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVFNVP 120
 DB 84 FLRRGIFPSHRDMNQVLDAVENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVFNVP 143
 QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFPSLDYMGSSGFYKN 180
 DB 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFPSLDYMGSSGFYKN 203
 QY 181 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 240
 DB 204 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 263
 QY 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQGAQTMSASDPNSIFLDTAKQIKT 300
 DB 264 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQGAQTMSASDPNSIFLDTAKQIKT 323
 QY 301 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
 DB 324 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383
 QY 361 KXALIEVLQPLIAEQAARKEVTDEIVKFEFMTPRKLSFDFQ 401
 DB 384 KXALIEVLQPLIAEQAARKEVTDEIVKFEFMTPRKLSFDFQ 424

RESULT 8

AAAG79547

ID AAG79547 standard; protein; 437 AA.

XX

AC AAG79547;

XX

DT 10-DEC-2002 (first entry)

XX

DE His6-tagged mini-TrpRS polypeptide.

XX

T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;
 KW neovascular eye disease; age-related macular degeneration;
 KW ocular complication; diabetes; rubroretic glaucoma; retinopathy;
 KW prematurity; keratitis; ischaemic retinopathy; sickle cell;
 KW pathological myopia; ocular histoplasmosis; pterygia;

KW puniate innerchorioidopathy; retinal degeneration; growth factor;
 KW vascularisation; vascular endothelial cell function; angiogenesis.
 XX Homo sapiens.
 OS
 PN WO200267970-A1.
 XX
 PD 06-SEP-2002.
 XX
 PF 22-FEB-2002; 2002WO-US005185.
 XX
 PR 23-FEB-2001; 2001US-0270951P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA Schimmel P, Wakasugi K, Friedlander M;
 PI
 XX WPI; 2002-698635/75.
 DR N-PSDB; ABA00329.
 DR
 XX New polypeptides derived from human tryptophanyl-tRNA synthase, useful
 PT for inhibiting ocular neovascularization in a patient, or for treating
 PT neovascular eye diseases, e.g. rubroretic glaucoma, retinopathy, keratitis,
 PT or pterygia.
 XX
 XX Example 3; Fig 1; 83pp; English.

This sequence represents a His6-tagged cleavage product, mini-TrpRS, of
 CC recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage
 CC product, T2, is water soluble and comprises residues 94-471 of full
 CC length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting
 CC ocular neovascularisation in a patient. The T2 polypeptide is useful for
 CC treating neovascular eye diseases, e.g. age-related macular degeneration,
 CC ocular complications of diabetes, rubroretic glaucoma, retinopathy of
 CC prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell),
 CC pathological myopia, ocular histoplasmosis, pterygia, or puniate
 CC innerchorioidopathy. This polypeptide is particularly useful for treating
 CC retinal degeneration to prevent the damaging effects of trophic and
 CC growth factors, and for promoting vascularisation to retard retinal
 CC degeneration by enhancing blood flow to cells. These are also useful for
 CC regulating vascular endothelial cell function, and in particular, for
 CC inhibiting angiogenesis

Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 5; Length 437;

Best Local Similarity 100.0%; Pred. No. 1.8e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60
 DB 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 83
 QY 61 FLRRGIFPSHRDMNQVLDAVENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVFNVP 120
 DB 84 FLRRGIFPSHRDMNQVLDAVENKPFYLYTGRGSSSEAMVGHILIPFTFKWLQDVFNVP 143
 QY 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFPSLDYMGSSGFYKN 180
 DB 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFFPSLDYMGSSGFYKN 203
 QY 181 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 240
 DB 204 VVKIQKHVTFNQKIGFIFGFTSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCA 263
 QY 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQGAQTMSASDPNSIFLDTAKQIKT 300
 DB 264 IDQDPYFRMTRDVA PRIGYPKALLHSTFFPALQGAQTMSASDPNSIFLDTAKQIKT 323
 QY 301 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
 DB 324 KVNKHAFFSGGRDTIEHRQFGNCNDVVSFMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383

QY 361 KKALIEVLQPLIAEHQARRKEVTDIEIVKFPMTPRKLSFDFQ 401
 Db 384 KKALIEVLQPLIAEHQARRKEVTDIEIVKFPMTPRKLSFDFQ 424

RESULT 9

ABU72385
 ID ABU72385 standard; protein; 437 AA.

AC ABU72385;
 XX
 DT 16-JUN-2003 (first entry)
 XX
 DE Human mini Tryptophanyl tRNA synthetase/His tag.
 XX
 KW Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic;
 KW vulnarary; Rossmann fold nucleotide binding domain; chemokine; EMAP II;
 KW vascular endothelial cell; solid tumour; myocardial infarction; enzyme;
 KW endothelial monocyte-activating polypeptide II; tumour metastasis;
 KW wound healing; dermal ulcer; endothelialisation; vascular graft surgery;
 KW abdominal wound; coronary bypass surgery; gene therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX US2002182666-A1.
 PN
 XX 05-DEC-2002.
 PD
 XX 21-MAR-2001; 2001US-00813718.
 XX
 PR 21-MAR-2001; 2001US-00813718.

XX (SCHZ/) SCHIMMEL P.
 XX (WAKA/) WAKASUGI K.

XX Schimmel P, Wakasugi K;
 PI
 XX WPI; 2003-340974/32.
 XX N-PSDB; ACA64106.

DR
 XX
 PT New truncated tryptophanyl-tRNA synthetase polypeptide comprising a
 PT Rossmann fold nucleotide binding domain or having chemokine activity
 PT useful for e.g. for regulating angiogenesis and for treating myocardial
 PT infarction.
 XX
 PS Example 1; Page 46-47; 91pp; English.

XX The invention relates to an isolated polypeptide comprising a truncated
 CC tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann
 CC fold nucleotide binding domain or having chemokine activity. The isolated
 CC polypeptide is capable of regulating vascular endothelial cell function.
 CC TrpRS has a C-terminal domain containing an EMAP II (endothelial monocyte
 CC -activating polypeptide II, a proinflammatory cytokine)-like domain and
 CC is similar in sequence to TrpRS. Also included are a polynucleotide
 CC encoding TrpRS (or a polynucleotide 95% similar to it) a TrpRS epitope,
 CC 5' and 3' deletions of the TrpRS polynucleotide, a recombinant vector
 CC comprising an isolated TrpRS nucleic acid, a recombinant host cell
 CC containing the TrpRS nucleic acid and expressing TrpRS, an isolated anti-
 CC TrpRS antibody, producing truncations of TrpRS by treating it with a
 CC protease, and suppressing angiogenesis, solid tumours or a condition that
 CC would benefit from decreased angiogenesis in a mammal by administering to
 CC the mammal the composition comprising the TrpRS truncated protein. The
 CC isolated polypeptide is useful for the preparation of a pharmaceutical
 CC composition for transdermal, transmucosal, enteral or parenteral
 CC administration. The truncated tRNA synthetase polypeptide is useful for
 CC research, diagnostic, prognostic and therapeutic applications. The tRNA
 CC synthetase are useful for regulating vascular endothelial cell function,
 CC particularly for regulating angiogenesis, for treating myocardial
 CC infarction and solid tumour, and for suppressing tumour metastasis.
 CC Angiogenic tRNA synthetase polypeptides are useful as wound healing
 CC agents or for treating full thickness wounds such as dermal ulcers, in
 CC the promotion of endothelialisation in vascular graft surgery, in the

CC treatment of abdominal wounds where there is a high risk infection, in
 CC conjunction with coronary bypass surgery by stimulating the growth of the
 CC transplanted tissue, and in gene therapy. The present sequence is a Trp
 CC tRNA synthetase protein (full length, truncated or mutant) with a His
 CC affinity tag
 XX
 SQ Sequence 437 AA;

Query Match 100.0%; Score 2116; DB 6; Length 437;
 Best Local Similarity 100.0%; Pred. No. 1.8e-209;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 60
 Db 24 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 83
 QY 61 FLRRGIFFFSHRDNNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIFFKWLQDVNPV 120
 Db 84 FLRRGIFFFSHRDNNQVLDAYENKKPFYLYTGRGSSSEAMHVGHILIPFIFFKWLQDVNPV 143
 QY 121 LVIQMTDDEKYLWKOLTLDAQYGDVAENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
 Db 144 LVIQMTDDEKYLWKOLTLDAQYGDVAENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 203
 QY 181 VKIQKHVTFNQVKGIFGFTSDSCIGKISFPALQAAPSFNSPQIFRDRDTIOCLIPCA 240
 Db 204 VKIQKHVTFNQVKGIFGFTSDSCIGKISFPALQAAPSFNSPQIFRDRDTIOCLIPCA 263
 QY 241 IDODPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSADPNSSIFLTDTAKQIKT 300
 Db 264 IDODPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSADPNSSIFLTDTAKQIKT 323
 QY 301 KVNKHAFFSGGRDTIEHRQFVGNCVDVVSFMYLTFLEDDDKLEQIRKDYTGAMLTGEL 360
 Db 324 KVNKHAFFSGGRDTIEHRQFVGNCVDVVSFMYLTFLEDDDKLEQIRKDYTGAMLTGEL 383
 QY 361 KKALIEVLQPLIAEHQARRKEVTDIEIVKFPMTPRKLSFDFQ 401
 Db 384 KKALIEVLQPLIAEHQARRKEVTDIEIVKFPMTPRKLSFDFQ 424

RESULT 10

ADF76576
 ID ADF76576 standard; protein; 471 AA.

XX
 AC ADF76576;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Novel human secreted and transmembrane protein SeqID 250.
 XX
 KW human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuropeptide; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 OS Homo sapiens.

XX WO2003072035-A2.
 PN
 XX
 PD 04-SEP-2003.
 XX
 PF 21-FEB-2003; 2003WO-US0005241.
 XX
 PR 22-FEB-2002; 2002US-0359461P.

XX (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;
 XX WPI; 2003-721702/68.
 DR

DR N-PSDB; ADF76575.

XX New PRO polypeptides, useful for diagnosing and treating an immune

PT related disorder, e.g. systemic lupus erythematosus, rheumatoid

PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or

PT diabetes mellitus.

XX

XX Claim 10; SEQ ID NO 250; 918pp; English.

XX

XX This invention relates to novel nucleic acids encoding human PRO secreted

CC and transmembrane proteins. Extracellular proteins play important roles

CC in the formation, differentiation and maintenance of multicellular

CC organisms. The fate of many individual cells (for example proliferation,

CC migration or differentiation) is typically governed by information

CC received from other cells and the immediate environment. The information

CC is often transmitted by secreted polypeptides (for example mitogenic

CC factors, survival factors, cytotoxic factors, differentiation factors,

CC neurotrophins and hormones), which are received and interpreted by diverse

CC cell receptors or membrane bound proteins. These membrane bound proteins

CC as in the blocking of receptor-ligand interactions. The current invention

CC provides the amino acid sequences of novel human membrane bound receptors

CC and proteins, along with the cDNA sequences encoding them. The novel

CC proteins of the invention may have cytosolic activities through the

CC stimulation of chondrocytes. The nucleic acids of the invention may be

CC useful for the manufacture of a medicament for diagnosing or treating a

CC tumour in a mammal. In addition, they may be useful for measuring or

CC detecting the expression of a tumour associated gene. The present

CC sequence is the amino acid sequence of a human PRO protein of the

CC invention.

XX

SQ Sequence 471 AA;

Query Match 100.0%; Score 2116; DB 7; Length 471;

Best Local Similarity 100.0%; Pred. No. 2.1e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 130

Qy 61 FLRGIFPSHRDNNQVLDAYENKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 120

Db 131 FLRGIFPSHRDNNQVLDAYENKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 190

Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFISDLDYMGSSGFYKN 250

Qy 181 VVKIQKHVTENVQKIGFDTSDCIGKISFPALQAPSFNSFPQIFRDRDTDIQCLIPCA 240

Db 251 VVKIQKHVTENVQKIGFDTSDCIGKISFPALQAPSFNSFPQIFRDRDTDIQCLIPCA 310

Qy 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFFPALQAGTQKMSASDPNSISFLTDTAKQIKT 300

Db 311 IDQDPYFRMTRDVA PRIGYPKALLHSTFFFPALQAGTQKMSASDPNSISFLTDTAKQIKT 370

Qy 301 KVNKHAFGSGRDTIEHRQFGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 371 KVNKHAFGSGRDTIEHRQFGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLAEHQARKEVTDEIVKEFMTPRKLSFDFQ 401

Db 431 KKALIEVLQPLAEHQARKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 11

ABU64298

ID ABU64298 standard; protein; 471 AA.

XX

AC ABU64298;

XX

DT 11-MAR-2004 (first entry)

Human tryptophanyl-tRNA synthetase protein.

Vector; rAAV; recombinant adeno-associated viral vector;

anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;

retinal degeneration; macular degeneration; neovascularisation;

ophthalmological.

Homo sapiens.

WO2003080648-A2.

02-OCT-2003.

20-MAR-2003; 2003WO-US008667.

20-MAR-2002; 2002US-0366114P.

(UYFL) UNIV FLORIDA RES FOUND INC.

(UYJO) UNIV JOHNS HOPKINS.

Hauswirth WW, Campochiaro PA, Berns KI;

WPI; 2003-779243/73.

N-PSDB; AAL56267.

Novel adeno-associated viral vector comprising polynucleotide encoding

pigment epithelium-derived factor, useful for treating choroidal

neovascularization, blindness, loss of vision.

Claim 14; Page 46; Opp; English.

The present invention relates to an adeno-associated viral (AAV) vector

comprising a polynucleotide that comprises a nucleic acid segment that

encodes a choroidal or ocular neovascularisation inhibitory polypeptide

operably linked to a promoter that expresses the segment to produce the

polypeptide in a selected mammalian host cell. Such a vector is useful

for providing a choroidal or ocular neovascularisation inhibitory

polypeptide to a mammal, for use in the therapy of ocular

neovascularisation, choroidal neovascularisation, retinal

neovascularisation, age-related macular degeneration, visual impairment,

ocular dysfunction, loss of vision, retinopathy, or blindness in a human.

The present sequence is a protein shown in the exemplification of the

invention

Sequence 471 AA;

Query Match 100.0%; Score 2116; DB 7; Length 471;

Best Local Similarity 100.0%; Pred. No. 2.1e-209;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 130

Qy 61 FLRGIFPSHRDNNQVLDAYENKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 120

Db 131 FLRGIFPSHRDNNQVLDAYENKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 190

Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFISDLDYMGSSGFYKN 250

Qy 181 VVKIQKHVTENVQKIGFDTSDCIGKISFPALQAPSFNSFPQIFRDRDTDIQCLIPCA 240

Db 251 VVKIQKHVTENVQKIGFDTSDCIGKISFPALQAPSFNSFPQIFRDRDTDIQCLIPCA 310

Qy 241 IDQDPYFRMTRDVA PRIGYPKALLHSTFFFPALQAGTQKMSASDPNSISFLTDTAKQIKT 300

Db 311 IDQDPYFRMTRDVA PRIGYPKALLHSTFFFPALQAGTQKMSASDPNSISFLTDTAKQIKT 370

Qy 301 KVNKHAFGSGRDTIEHRQFGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360

Db 371 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 12

ID ADN39916

ADN39916 standard; protein; 471 AA.

XX AC ADN39916;

XX DT 17-JUN-2004 (first entry)

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C286.

XX DE Human; differential expression; cancer; angiogenic disorder;

XX DE fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

XX DE inflammatory disease; autoimmune disease;

XX DE retinal neovascularisation syndrome; scarring; uterine fibroid;

XX DE detection; diagnosis; prognosis; drug screening; drug targeting;

XX DE wound healing; contraception; cytostatic; cardiac; immunomodulatory;

XX DE vulnary; gene therapy; vaccine.

OS Homo sapiens.

XX PN WO2003042661-A2.

XX PD 22-MAY-2003.

XX PF 13-NOV-2002; 2002WO-US036810.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 21-NOV-2001; 2001US-0332464P.

XX PR 29-NOV-2001; 2001US-0334393P.

XX PR 03-DEC-2001; 2001US-0335394P.

XX PR 14-DEC-2001; 2001US-0340376P.

XX PR 08-JAN-2002; 2002US-0347211P.

XX PR 10-JAN-2002; 2002US-0347349P.

XX PR 08-FEB-2002; 2002US-0355250P.

XX PR 13-FEB-2002; 2002US-0356714P.

XX PR 20-FEB-2002; 2002US-0359077P.

XX PR 23-MAR-2002; 2002US-0368809P.

XX PR 04-APR-2002; 2002US-0370110P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PR 05-JUN-2002; 2002US-0386614P.

XX PR 16-JUL-2002; 2002US-0396839P.

XX PR 22-JUL-2002; 2002US-0397775P.

XX PR 22-JUL-2002; 2002US-0397845P.

XX PR 09-SEP-2002; 2002US-0409450P.

XX PA (BOSB-) EOS BIOTECHNOLOGY INC.

XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

XX PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX DR WPI; 2003-468649/44.

XX DR N-PSDB; ADN39699.

XX PT Determining the presence or absence of a pathological cell in a patient,

XX PT useful for diagnosing, prognosing or treating cancer, comprises detecting

XX PT a nucleic acid in a biological sample.

XX PS Claim 12; SEQ ID NO C286; 1385pp; English.

XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

XX CC whose expression is upregulated or downregulated in specific cancers or

XX CC other diseases such as angiogenic or fibrotic disorders, and to methods

XX CC of determining the presence or absence of a pathological cell in a

XX CC patient by detecting a nucleic acid at least 80% identical to those of

XX CC the invention or by detecting a polypeptide of the invention. The

XX CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a

CC polypeptide of the invention; use of such antibodies for drug targeting;

CC and methods of screening for modulators of activity or expression of the

CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

CC antibodies and methods are useful for diagnosing, prognosing and treating

CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may

CC also be useful in wound healing and in contraception. The present

CC sequence represents a polypeptide of the invention.

XX XX Sequence 471 AA;

Qy 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60

Db 71 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130

Qy 61 FLRRGIFFSHRDMNQVLDAVENKPPVLYTGRGPPSEAMHVGHLIPFIFTKWLQDVNP 120

Db 131 FLRRGIFFSHRDMNQVLDAVENKPPVLYTGRGPPSEAMHVGHLIPFIFTKWLQDVNP 190

Qy 121 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180

Db 191 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 250

Qy 181 VKIQKHVTPNQVKGIFGFTDSDCIKISPPAIQAAPSPNSPQIFRDRDTQCLIPCA 240

Db 251 VKIQKHVTPNQVKGIFGFTDSDCIKISPPAIQAAPSPNSPQIFRDRDTQCLIPCA 310

Qy 241 IDODPYFRMTRDVA PRIGYPKALLHSTFPALQGAQTKMSASDPNSSIFLTDATAKQIKT 300

Db 311 IDODPYFRMTRDVA PRIGYPKALLHSTFPALQGAQTKMSASDPNSSIFLTDATAKQIKT 370

Qy 301 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360

Db 371 KVNKHAFFSGGRDTEIEHRQFGGNCVDVSPFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401

Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 13

ID ADJ75318 standard; protein; 471 AA.

XX AC ADJ75318;

XX DT 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:570.

XX DE bronchial asthma; chronic obstructive pulmonary disease;

XX DE respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

XX DE gene therapy; marker.

XX OS Homo sapiens.

XX PN EP1394274-A2.

XX PD 03-MAR-2004.

XX PF 04-AUG-2003; 2003EP-00254857.

XX PR 06-AUG-2002; 2002JP-00229312.

XX PR 20-MAR-2003; 2003JP-00077212.

XX PA (GENO-) GENOX RES INC.

QY 181 VVKIQHVTNQVKGIFGFTDSDCIGKISFPALQAAAPSFNSFPQIFPRDRTDIOCLIPCA 240
DB 251 VVKIQHVTNQVKGIFGFTDSDCIGKISFPALQAAAPSFNSFPQIFPRDRTDIOCLIPCA 310
QY 241 IDQDPYFRMTRDVA PRIGYKPKALLHSTFPALQGAQTAKMSADPNSSIFLDTAKQIKT 300
DB 311 IDQDPYFRMTRDVA PRIGYKPKALLHSTFPALQGAQTAKMSADPNSSIFLDTAKQIKT 370
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
DB 371 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
QY 361 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 401
DB 431 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 15
AAB47615
ID AAB47615 standard; protein; 484 AA.
XX
AC AAB47615;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human full-length TrpRS.
XX
KW Tyrosyl-tRNA synthetase; TrpRS; Rosemann fold nucleotide binding domain;
KW vascular endothelial cell function; burn; plastic surgery; abdomen;
KW polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
KW angiogenesis; graft; myocardial infarction; solid tumour; wound healing;
KW dermal ulcer; diabetic ulcer; endothelialization;
KW tyriophanyl-tRNA synthetase; trpRS; vascular graft surgery.
XX
OS Homo sapiens.
XX
PN WO200174841-A1.
XX
PD 11-OCT-2001.
XX
XX 21-MAR-2001; 2001WO-US008966.
XX
XX 31-MAR-2000; 2000US-0193471P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Schimmel P, Wakaesugi K;
XX
XX WPI; 2001-626377/72.
DR N-PSDB; AAH43602.
XX
XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating
PT vascular endothelial function, in particular for regulating angiogenesis,
PT tumor metastasis and treating myocardial infarction.
XX
PS Disclosure; Page 117-19; 150pp; English.
XX
XX The sequences given in AAB47615-18 show full length and truncated
CC versions of tyriophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of
CC the invention comprises a Rosemann fold nucleotide binding domain, and is
CC capable of regulating vascular endothelial cell function. It is of
CC approx. 40 kilo Dalton molecular weight and is produced by cleavage of
CC full length TrpRS with polymorphonuclear leucocyte elastase. Truncated
CC TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing
CC angiogenesis to a graft, treating myocardial infarction, solid tumor, and
CC a condition that would benefit from increased or decreased angiogenesis
CC in a mammal, in particular humans. It is also useful in diagnosis and as
CC a wound healing agent for treating wounds such as dermal ulcers, diabetic
CC ulcers, burns and injuries and in plastic surgery when reconstruction is
CC required following a burn or for cosmetic purposes. It is particularly
CC useful in the treatment of abdominal wounds where there is high risk of
CC infection. Truncated TrpRS promotes endothelialization in vascular graft
CC surgery and is used in conjunction with angiography to administer the

CC angiogenic trNA synthetase polypeptides or polynucleotides directly to
CC the lumen and wall of the blood vessel
XX
SQ Sequence 484 AA;
Query Match 100.0%; Score 2116; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.1e-209;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP HH 60
DB 71 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP HH 130
QY 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLTGRGPFSSSEAMHVGHILPFIPTKWLQDVFNVP 120
DB 131 FLRRGIFFSHRDMNQVLDAYENKKPFYLTGRGPFSSSEAMHVGHILPFIPTKWLQDVFNVP 190
QY 121 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFISDLDMGSSGGFYKN 180
DB 191 LVIQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFISDLDMGSSGGFYKN 250
QY 181 VVKIQHVTNQVKGIFGFTDSDCIGKISFPALQAAAPSFNSFPQIFPRDRTDIOCLIPCA 240
DB 251 VVKIQHVTNQVKGIFGFTDSDCIGKISFPALQAAAPSFNSFPQIFPRDRTDIOCLIPCA 310
QY 241 IDQDPYFRMTRDVA PRIGYKPKALLHSTFPALQGAQTAKMSADPNSSIFLDTAKQIKT 300
DB 311 IDQDPYFRMTRDVA PRIGYKPKALLHSTFPALQGAQTAKMSADPNSSIFLDTAKQIKT 370
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
DB 371 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
QY 361 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 401
DB 431 KKALIEVLQPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 471

Search completed: January 10, 2005, 21:19:43
Job time : 157 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:14:03 ; Search time 40 Seconds
(without alignments)
964.573 Million cell updates/sec

Title: US-09-813-718-10_COPY_71_471
Perfect score: 2116
Sequence: 1 SNHGPDTEAEEDFVDPWTV.....VTDEIVKFTPRKLSDFDQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2101	99.3	471	1 A41706	tryptophan-tRNA li
2	2028.5	95.9	475	1 YWBO	tryptophan-tRNA li
3	1946.5	92.0	475	1 YWRBR	tryptophan-tRNA li
4	1938	91.6	481	2 S50053	tryptophan-tRNA li
5	1210	57.2	395	2 S58157	hypothetical prote
6	1163	55.0	432	2 S51901	tryptophan-tRNA li
7	907	42.9	386	2 C90190	tryptophanyl-tRNA
8	803	37.9	385	2 C75020	tryptophanyl-tRNA
9	626.5	29.6	301	2 G71206	tryptophan-tRNA li
10	534.5	25.3	380	2 G84372	tryptophanyl-tRNA
11	409.5	19.4	370	2 E64476	tryptophan-tRNA li
12	397.5	18.8	364	2 E69131	tryptophan-tRNA li
13	386	18.2	134	2 T43806	tryptophan-tRNA li
14	370.5	17.5	420	2 E69461	tryptophanyl-tRNA
15	353	16.7	374	2 D72477	probable tryptopha
16	269.5	12.7	513	2 F84373	tryptophanyl-tRNA
17	192	9.1	323	2 H69346	tyrosyl-tRNA synth
18	188	8.9	364	2 E72512	probable tyrosyl-t
19	185.5	8.8	341	2 D95260	tryptophanyl-tRNA
20	185.5	8.8	341	2 G98125	tryptophan-tRNA li
21	174.5	8.2	341	2 B86633	tryptophan-tRNA li
22	172	8.1	394	2 A45999	tyrosine-tRNA liga
23	170.5	8.1	366	2 S75410	tyrosine-tRNA liga
24	169	8.0	395	2 H70385	tryptophan-tRNA li
25	167	7.9	351	2 E75438	tryptophanyl-tRNA
26	166.5	7.9	346	2 B71496	tryptophan-tRNA li
27	164.5	7.8	895	2 A86410	protein F3M18.22 [
28	163.5	7.7	353	2 E70100	tryptophan-tRNA li
29	163	7.7	460	2 C84750	probable tyrosyl-t

RESULT 1

A41706

tryptophan-tRNA ligase (EC 6.1.1.2) [similarity] - human

N;Alternate names: interferon-inducible protein IFF53; peptide-chain release factor homo

C;Species: Homo sapiens (man)

C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004

C;Accession: A41633; A41706; S19246; JN0676; JH0533; S26287

R;Fleckner, J.; Rasmussen, H.H.; Justesen, J.

Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991

A;Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma

A;Reference number: A41633; MUID:92107982; PMID:1763065

A;Accession: A41633

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-471 <FLE>

A;Cross-references: UNIPROT:P23381; GB:X59892; NID:g30820; PIDN:CAA42545.1; PID:g30821

R;Rubin, B.Y.; Anderson, S.L.; King, L.; Powell, R.J.; Tate, W.P.

J. Biol. Chem. 266, 24245-24248, 1991

A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts

A;Reference number: A41706; MUID:92105071; PMID:1761529

A;Accession: A41706

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-471 <RUB>

A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657

R;Buwitt, U.; Flohr, T.; Boettger, E.C.

EMBO J. 11, 489-496, 1992

A;Title: Molecular cloning and characterization of an interferon induced human cDNA with

A;Reference number: S19246; MUID:92164636; PMID:1537332

A;Accession: S19246

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-423, 'R', 425-471 <BUW>

A;Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA44450.1; PID:g32709

A;Note: 213-Ser and 214-Tyr were also found

R;Frolova, L.Y.; Grigorjeva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.

Gene 128, 237-245, 1993

A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response element

A;Reference number: JN0676; MUID:93292992; PMID:7685728

A;Accession: JN0676

A;Molecule type: DNA

A;Residues: 1-141;182-471 <FRO1>

A;Cross-references: GB:X67918; GB:S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; GB:X6

4; NID:g37974; GB:X67925; GB:S62855; NID:g37975; GB:X67926; GB:S62856; NID:g37976; GB:X6

A;Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 3

R;Frolova, L.Y.; Grigorjeva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.

Gene 109, 291-296, 1991

A;Title: Cloning and nucleotide sequence of the structural gene encoding for human trypt-

A;Reference number: JH0533; MUID:92112058; PMID:1765274

A;Accession: JH0533

A;Molecule type: mRNA

C;Keywords: aminocacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;24-69/Domain: amino acid-tRNA ligase repeat homology <ATL>
Query Match 95.9%; Score 2028.5; DB 1; Length 475;
Best Local Similarity 95.8%; Pred. No. 4.6e-156; Indels 1; Gaps 1;
Matches 384; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60
DB 76 SEGLDATEADDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELVNRIERATGQRP 135
QY 61 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFIPTFKWLQDV 120
DB 136 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFIPTFKWLQDV 195
QY 121 LVITQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 180
DB 196 LVITQMTDDKYLWKDLTLDOAYGDAVENAKD-ITCGFDINKTFIFSDLDYMGSSGFY 254
QY 181 VKIKQHVTFNQVKGIFGFTSDSDICIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 240
DB 255 VKIKQHVTFNQVKGIFGFTSDSDICIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 314
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTDTA 300
DB 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTDTA 374
QY 301 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFFLEDDDKLEIRKDYTSGLMTG 360
DB 375 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFFLEDDDKLEIRKDYTSGLMTG 434
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKPFMTPRKLSFDFQ 401
DB 435 KKALIEVLQPLIAEHQARRKEVTDEIVKPFMTPRKLSFDFQ 475

RESULT 3
YWBO
tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - rabbit
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 13-Feb-1998 #text_change 03-Jun-2002
C;Accession: A35904; S37396
R;Lee, C.C.; Craigen, W.J.; Muzny, D.M.; Harlow, E.; Caskey, C.T.
Proc. Natl. Acad. Sci. U.S.A. 87, 3508-3512, 1990
A;Title: Cloning and expression of a mammalian peptide chain release factor with sequence
A;Reference number: A35904; MUID:90239043; PMID:2185472
A;Accession: A35904
A;Molecule type: mRNA
A;Residues: 1-475 <LSE>
A;Cross-references: GB:M33460
R;Frolova, L.Y.; Dalphin, M.E.; Justesen, J.; Powell, R.J.; Druegon, G.; McCaughan, K.K.;
EMBO J. 12, 4013-4019, 1993
A;Title: Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are
A;Reference number: S37396; MUID:94009008; PMID:8404867
A;Accession: S37396
A;Molecule type: mRNA
A;Residues: 166-177 <PRO>
C;Genetics:
A;Gene: WRS
C;Complex: homodimer [validated, MUID:94009008]
C;Function:
A;Description: EC 6.1.1.2 [validated, MUID:94009008]; catalyzes the ATP-dependent format
A;Note: mammalian WRS (tryptophanyl-tRNA synthetases) and eRF (polypeptide chain release
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminocacyl-tRNA synthetase; ATP; homodimer; ligase; metalloprotein; protein b
F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>
F;174-177/Region: ATP-binding motif (HXGH)

Query Match 92.0%; Score 1946.5; DB 1; Length 475;
Best Local Similarity 90.8%; Pred. No. 1.9e-149;
Matches 364; Conservative 21; Mismatches 15; Indels 1; Gaps 1;

A;Residues: 1-212, 'GD', 215-471 <PRO2>
A;Cross-references: GB:M61715; NID:G340367; PIDN:AAA61298.1; PID:G340368
A;Experimental source: fibroblast
C;Genetics:
A;Gene: GDB:WARS; IFP53
A;Cross-references: GDB:119632; OMIM:191050
A;Map position: 14q23-14q31
A;Introns: 33/3; 105/1; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminocacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;113-64/Domain: amino acid-tRNA ligase repeat homology <ATL>
Query Match 99.3%; Score 2101; DB 1; Length 471;
Best Local Similarity 99.5%; Pred. No. 6.2e-162; Indels 0; Gaps 0;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 60
DB 71 SNHGPDTEAEEDFVDPMTVTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQRP 130
QY 61 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFIPTFKWLQDV 120
DB 131 FLRRGIFFSHRDMNQVLDAVENKPFYLYTGRGSSSEAMHVGHLPFIPTFKWLQDV 190
QY 121 LVITQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 180
DB 191 LVITQMTDDKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFY 250
QY 181 VKIKQHVTFNQVKGIFGFTSDSDICIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 240
DB 251 VKIKQHVTFNQVKGIFGFTSDSDICIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIP 310
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTDTA 300
DB 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQAGTQKMSASDPNSSIFLTDTA 370
QY 301 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFFLEDDDKLEIRKDYTSGLMTG 360
DB 371 KVNKHAFSGGRDTIEHRQFGNCVDVVSFMYLTFFLEDDDKLEIRKDYTSGLMTG 430
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKPFMTPRKLSFDFQ 401
DB 431 KKALIEVLQPLIAEHQARRKEVTDEIVKPFMTPRKLSFDFQ 471

RESULT 2
YWBO
tryptophan-tRNA ligase (EC 6.1.1.2) [validated] - bovine
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A40279; JN0354; S10460; S14540
R;Garret, M.; Pajot, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedet
Biochemistry 30, 7809-7817, 1991
A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic
A;Reference number: A40279; MUID:91329348; PMID:1907847
A;Accession: A40279
A;Molecule type: mRNA
A;Residues: 1-475 <GAR>
A;Cross-references: UNIPROT:P17248; GB:M74074; EMBL:X53918; NID:G163798; PIDN:AAA30799.1
A;Experimental source: pancreas
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue
R;Zargaro, T.A.; Kovaleva, G.K.; Favorova, O.O.; Aevina, H.B.; Telezhinskaya, I.H.
Bioorg. Khim. 15, 1307-1311, 1989
A;Title: Amino acid sequence of several peptides of tryptophanyl-tRNA synthetase from ca
A;Reference number: JN0354; MUID:90211408; PMID:2631684
A;Accession: JN0354
A;Molecule type: protein
A;Residues: 112-124,282-287, 'N', 288, 'F', 289-292, 'Q', 293-294, 'IR', 336-353,423-441,443-449
A;Experimental source: liver
A;Note: this paper is in Russian
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

QY 2 NHG-PDATEAEEDVDWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 60
DB 75 SHGDPEAVDDKDFVDWVTQTSSAKGIDYDKLIVQFGSSKIDKELYNRIERATGQRP 134
QY 61 FLRRGIFFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 120
DB 135 FLRRGIFFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 194
QY 121 LVQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGPGYKN 180
DB 195 LVQMSDDEKYLWKDLTLEQVYGVYTLNENAKDIMPFGDVNKTFFISDLDYMGSSGPGYKN 254
QY 181 VKIQKHVTNNOVKIGIFGFTDSDCIGKISFPALQAAPSFNSFPQIFRDRDTDIOCLIPCA 240
DB 255 VKIQKHVTNNOVKIGIFGFTDSDCIGKISFPALQAAPSFNSFPQIFRDRDTDIOCLIPCA 314
QY 241 IDQDPYFRMTRDVAAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAQIKT 300
DB 315 IDQDPYFRMTRDVAAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAQIKT 374
QY 301 KVNKAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 360
DB 375 KVNKAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYSSGAMLTGEL 434
QY 361 KXALIEVLQPLIAHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
DB 435 KXELIDVLQPLVAHQARRKEVTDEMVKFMTPRQLCFHYQ 475
RESULT 4
S50053
tryptophan-tRNA ligase (BC 6.1.1.2) alpha-2 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S50053; S50052; I49391; S31461; S31462
R;Paot, B.; Sarger, C.; Bonnet, J.; Garret, M.
J. Mol. Biol. 242, 599-603, 1994
A;Title: An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase
A;Reference number: S50052; MUID: 95018226; PMID: 7932716
A;Accession: S50053
A;Molecule type: mRNA
A;Residues: 1-481 <PAJ>
A;Cross-references: UNIPROT: P32921; EMBL: X69657; NID: g55437; PIDN: CAA49348.1; PID: g55438
A;Genetics: LSF
A;Note: Intron position was determined by sequencing of genomic DNA
A;Accession: S50052
A;Molecule type: mRNA
A;Residues: 1-475 <PAW>
A;Cross-references: EMBL: X69656; NID: g55435; PIDN: CAA49347.1; PID: g55436
A;Genetics: SSF
R;Kisselev, L.L.
Biochimie 75, 1027-1039, 1993
A;Title: Mammalian tryptophanyl-tRNA synthetases.
A;Reference number: I49391; MUID: 94257729; PMID: 7515282
A;Accession: I49391
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-481 <RES>
A;Cross-references: EMBL: X69657; NID: g55437; PIDN: CAA49348.1; PID: g55438
C;Genetics: <LSF>
A;Gene: WRS
A;Introns: 475/2
A;Note: the list of introns may be incomplete; clone W13
C;Genetics: <SSF>
A;Gene: WRS
A;Note: clone S5
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: alternative splicing; aminoacyl-tRNA synthetase; ligase; protein biosynthesis
F;1-481/Product: tryptophan-tRNA ligase alpha-2 chain long splice form #status predicted
F;1-475/Product: tryptophan-tRNA ligase alpha-2 chain short splice form #status predicted
F;23-68/Domain: amino acid-tRNA ligase repeat homology <ATL>
Query Match 91.6%; Score 1938; DB 2; Length 481;

Best Local Similarity 90.8%; Pred. No. 9.6e-149;
Matches 363; Conservative 21; Mismatches 16; Indels 0; Gaps 0;
QY 2 NHG-PDATEAEEDVDWVTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 61
DB 76 NCDSDATKASEDFVDWVTQTSSAKGIDYDKLIVQFGSSKIDKELINRIERATGQRP 135
QY 62 LRGRIFFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 121
DB 136 LRGRIFFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 195
QY 122 VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGPGYKN 181
DB 196 VIQMSDDEKYLWKDLTLEQAYSVTVENAKDIIACGFDINKTFIFSDLDYMGSSGPGYKN 255
QY 182 VKIQKHVTNNOVKIGIFGFTDSDCIGKISFPALQAAPSFNSFPQIFRDRDTDIOCLIPCA 241
DB 256 VKIQKHVTNNOVKIGIFGFTDSDCIGKISFPALQAAPSFNSFPQIFRDRDTDIOCLIPCA 315
QY 242 DQDPYFRMTRDVAAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAQIKT 301
DB 316 DQDPYFRMTRDVAAPRIGYKPKALLHSTFFPALQGAOTKMSADPNSSIFLTDTAQIKT 375
QY 302 KVNKAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 361
DB 376 KVNKAFSGGRDITIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL 435
QY 362 KXALIEVLQPLIAHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
DB 436 KXELIDVLQPLVAHQARRKEVTDEMVKFMTPRQLCFHYQ 475
RESULT 5
S58157
hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58157; T38561
R;Gentles, S.; Churcher, C.M.
submitted to the EMBL Data Library, July 1995
A;Reference number: S58145
A;Accession: S58157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <GEN>
A;Cross-references: UNIPROT: Q09692; EMBL: Z50142; NID: g1052783; PIDN: CAA90500.1; PID: g10528
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z21799
A;Accession: T38561
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-395 <GE2>
A;Cross-references: EMBL: Z50142; PIDN: CAA90500.1; GSPDB: GN00066; SPDB: SPAC2F7.13c
A;Experimental source: strain 972h-; cosmid c2F7
C;Genetics:
A;Gene: SPDB: SPAC2F7.13c
A;Map position: 1
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
Query Match 57.2%; Score 1210; DB 2; Length 395;
Best Local Similarity 59.6%; Pred. No. 5e-90;
Matches 235; Conservative 60; Mismatches 91; Indels 8; Gaps 4;
QY 11 EEDFVDPWVTQTS----SAKGIDYDKLIVRGSSKIDKELINRIERATGQRP 66
DB 4 EEQVTFVDPWVKGSIVDGEKIDYERLIVQFGTRKKTPEQLERFEKLTGKKPHLLLRGA 63
QY 67 FFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 126
DB 64 FFSHRDMMQVLDAYENKKPFYLYTGRGSSSEAMVGHILIPFIETKWLQDVFNVP 123
QY 127 DDEKYLWKO-LTLQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGPGYKN 185


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Db 124 DDEKFLKQGVSLDCORFARENADKIIAAGVDFPKTKTFIEMNSTYVG--GAFYQNVVRIA 181
QY 186 KHVTENQVKGIFGFTSDCTGKISFPFAIAAPSFNSFPQIFRDRDTIOCLICADDDP 245
Db 182 KCITANQSKACFGFTSDSISGKIHFASIQAAAPSFSSFPFHIFNGAKDIPCLICADDDP 241
QY 246 YFRMTRDVAIRIGYKPKALLHSTFFPALQAGATKMSASDPSNSTFLDTAKQIKTKVKNKH 305
Db 242 YFRLTRDVSGLRKFPPKALLHSTFFPALQAGATKMSASDPSNSTFLDTAKQIKTKVKNKH 301
QY 306 AFSGGRDTIEHRQFGNGCDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALI 365
Db 302 AFSGGGNTIIEHREKNGPVDVAYQVLSFFLDDDEKLKQLYNTYKAGTILSTGEMGECI 361
QY 366 EVLQPLIAEHQARKEVTDIEIVKEFMT-PRKLSF 398
Db 362 KLLIQFVSDFOARSKVDEATLDMFMDGSRKLEW 395

RESULT 6
S51901
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including
and a Delta.
A;Reference number: S51948
A;Accession: S51901
A;Molecule type: DNA
A;Residues: 1-432 <VAN>
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the
a delta element.
A;Reference number: S59156; MUID:96076631; PMID:7502582
A;Accession: S59177
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-432 <VAN>
A;Cross-references: EMBL:Z48149; NID:9663234; PIDN:CAA88164.1; PID:9663256
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66791
A;Accession: S66793
A;Molecule type: DNA
A;Residues: 1-432 <DUR>
A;Cross-references: EMBL:Z74839; NID:G1419947; PIDN:CAA99110.1; PID:G1419948; GSPDB:GN00
A;Experimental source: strain 6288C
C;Genetics:
A;Gene: SGD:WRS1; WRS1: MIPS.YOL097C
A;Cross-references: SGD:S0005457
A;Map position: 15L
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: ligase
F;117-120/Region: ATP-binding motif (HXGH)

Query Match 55.0%; Score 1163; DB 2; Length 432;
Best Local Similarity 54.8%; Pred. No. 3.6e-86;
Matches 217; Conservative 71; Mismatches 100; Indels 8; Gaps 3;

QY 7 ATEAEDFVDPWT-----QTSSAKGIDYKLIIVRFGSSKIDKELINRIERATGQRPHF 61
Db 19 STDVKEQVTTWDEGGVDEOGRAGNIDYKLIQFGTKPNEETLKQFKQVTRGPEPHF 78
QY 62 LRRGIFSHRDMNQVLDAYENKKPFYLYTGRGPSEAMHGHLPFIPTKMLQDVFNVL 121

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Db 79 LRKGLFFSRDEFTKILDLYEQGKPFYLYTGRGPSSDMHGLHMIPEVFTKMLQEVDFVPL 138
QY 122 VTQMTDDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKN 180
Db 139 VIELTDDKFLFKHKTUINDVKNFARENADKIIAVGFDPKNTFIFSDLDYMG--GAFYET 196
QY 181 VKIQKHVTFNQVKGIFGFTSDCTGKISFPFAIAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 197 VVRVSQITGSTAKAVFGFNDSDCTGKGFHAFASIQATAFSPFPNVGLGLPDKTPCLIPCA 256
QY 241 IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQAGATKMSASDPSNSTFLDTAKQIKT 300
Db 257 IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQAGATKMSASDPSNSTFLDTAKQIKT 316
QY 301 KVNKHAFFSGGRDTIEHRQFGNGCDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
Db 317 KINKYAFSGGGQVSADLHRELGNPDVDVAYQVLSFFLDDDDVFLKECYDKYKSGELLSGEM 376
QY 361 KKALIEVLQPLIAEHQARKEVTDIEIVKEFMTPRKL 396
Db 377 KKLCTIETLQEFVKAFQERRAQVDEETLDFKFMVBHKL 412

RESULT 7
C90190
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: C90190
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.W.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <KUR>
A;Cross-references: GB:AE006641; NID:G13813608; PIDN:AAK40778.1; GSPDB:GN00155
C;Genetics:
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 42.9%; Score 907; DB 2; Length 386;
Best Local Similarity 48.6%; Pred. No. 1.5e-65;
Matches 191; Conservative 68; Mismatches 110; Indels 24; Gaps 10;

QY 8 TEAEDFVDPWTQVTSAGK-IDYDKLIIVRFGSSKIDKELINRIERATGQRPHF 66
Db 6 TMDPEFTVTPWEV-----KGKVDYDKLIIVGFGTKITEKLRKLNLAGDL-HVMLERNV 59
QY 67 FFSHRDMNQVLDAYENKKPFYLYTGRGPSEAMHGHLPFIPTKMLQDVFNVLQVMT 126
Db 60 FFSHRDLQVLDVNDYKSGFPLYTGRAPSL-GMHGHLIPIFTKMLQEFNANLYEIT 118
QY 127 DDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKNVYKIQ 185
Db 119 DDEKYNRPFTLDQTFESWAYNDLIIAAGFNPDKTFIFQDTEYI---RNMYPITVKIA 175
QY 186 KHVTENQVKGIFGFTSDCTGKISFPFAIAAPSFNSFPQIFRDRDTIOCLICADDDP 245
Db 176 KLLTFSEVRATFGDLASSNIGLIFYPALQIAPT-----MFEKK---RCLIPAGIDDDP 225
QY 246 YFRMTRDVAIRIGYKPKALLHSTFFPALQAGATKMSASDPSNSTFLDTAKQIKTKVKNKH 305
Db 226 YRLQRIASLGGYKAAQHSKFLPLTQEGKSSNPETAIIYLVDDPKYVERKIMKY 285
QY 306 AFSGGRDTIEHRQFGNGCDVDSFMYLTFFLEDDDD-KLQIRKDYTSGAMLTGELKKAL 364
Db 286 AFSGGQFTIELHRKYGNPBIDVPFQWLYYFFEEDDNRIKEIEBEYRSGKMLTGELKQIL 345
QY 365 IEVLQPLIAEHQARKEVTDIEIVKEFMTPRKLS 397

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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1921
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 29.6%; Score 626.5; DB 2; Length 301;
Best Local Similarity 44.2%; Pred. No. 5e-43;
Matches 134; Conservative 56; Mismatches 92; Indels 21; Gaps 7;

Qy 99 MHVGHLLPFTTKWLQDVFNPLVLTQMTDDEKYLWKD-LTLQAYGDADAVENAKDIITACGF 157
Db 1 MHIGHIIPFATKWLQSKFGVNLVIQITDDEKFLPKNLTFTDTRKWAYDNLIDIIAVGF 60
Qy 158 DINKTFISDLIDYMGSSGFYKNVYKIQHVTFNQVKGIFGTDSDCIGKISFPAIQAAP 217
Db 61 DPDKTFIFQNSEF---TKIYEMAIPAKINFSMAKAVFGFTEQSKIGMIFPAIQIAP 116
Qy 218 SFNSNFPQIFRDRDIOCLIPCAIDQDPYFRWTRDVAPRIGYPKPALHSTFPFALOGAQ 277
Db 117 TF-----FERK---RCLIPAAIDQDPYWLQDRFAESLGYGYKTAALSHSKFVPSLTSL 166
Qy 278 TKMSASDPNSSIFLTDATAKQIKTKVKNHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFFEL 337
Db 167 GMSASAPETAIYLTDSPEDEVKKWKTLLTGGRTLKEQREKGEPEKCVFKWLEIFF 226
Qy 338 EDDDKLRQIRKDY---TSGAMLTGELKKALIEVLQPLAEHQARKEVTDIVKEFWMTPR 394
Db 227 EEDDK--KLKERYACKNGELTGCSEKYLISKIEFLKEHQRRKK-AEKLVEKPKYTG 283
Qy 395 KLS 397
Db 284 KLA 286

RESULT 10
G84373
tryptophanyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84373
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li,
A.;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: UNIPROT_Q9HN66; GB:AE004437; NID:g10581646; PIDN:AAG20355.1; GSPDB:G1;
C;Genetics:
A;Gene: trpS2
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology

Query Match 25.3%; Score 534.5; DB 2; Length 380;
Best Local Similarity 35.4%; Pred. No. 1.9e-35;
Matches 141; Conservative 76; Mismatches 140; Indels 41; Gaps 17;

Qy 10 AEEDFVDPWTQTSASGIDYDKLIVRGSSKIDKELINRIERATGQRPHFLRRGIFFS 69
Db 3 ADGNDVTPYAVESDD---LDYEKLARFGADELTDQARFP-----DHPLVNRGLFYA 53
Qy 70 HRDMQNVLDAYENKKPFYLYTGRGPSSAMVGHILPIFTKWLQDVFNPLVIQMTDDE 129
Db 54 GRDVDDFLTAGEQS---IVTGVGPGS-PHILGHAMVYFARRLQDEFGARVVVPLSDDE 108
Qy 130 KYLWKDLTLQOAYDAVE-NAKDIITACGFINDKTIFF---SPLDYM-GNSSGFYKVVVKI 184
Db 109 KYWFKQDTPAET-GDYLRANLRDLAVGDFDELTRIVVDTRDADVLVPLATAPAGDV--- 164

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QY 185 QKHTVFNQVKGIRGFTDSDICIGKISRPAPAIQAAPSFNSFPQIFRDRDITDIOCLIPCAIDQD 244
Db 165 -RHATLQNVVG-----EPDNGVGAFFAVQTAHL-----LPQLVHG--EHTLVPVIAVDQD 213
QY 245 PYFRMTRDVAPRIGYP--KPALLHSTFPFALQAGTQMSASDPNSISFLTDTAKQIKTKV 302
Db 214 PHVRSRDAVAKARYPVGKFGALLMQFLPSLAG-PGRWSSS-AGVSIRLTDSPDVTREKV 271
QY 303 NKHAFSGGRDTIEHROFGGNCVDVDSFMYLTFPLEDD-KLQIRKDYTSGLMGTGLX 361
Db 272 RTHAYTGRASVEHRAKGVPAEDVPFQYLSAFFEPDDAELARIERYRAGLLSGELX 331
QY 362 KALIEVLQPLIAEHOARKEVTDEIVKEMTPKLSFD 399
Db 332 DLAADRITFLAHQORRAALGD--VTEALDAFLRITDD 367

RESULT 11
F64476
Methanococcus jannaschii
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: F64476
R;Smith, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
; Reich, C.I.; Sadov, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64476
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-370 <BL>
A;Cross-references: UNIPROT:Q58810; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1;
A;Map position: FOR1375885-1376997
A;Start codon: GTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 19.4%; Score 409.5; DB 2; Length 370;
Best Local Similarity 30.9%; Pred. No. 2.3e-25;
Matches 119; Conservative 72; Mismatches 153; Indels 41; Gaps 16;

17 PWTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQPHPLRRGIFFSHRDNNQV 76
8 PW--ETPAV--IDYKKTMEQGVKPIVDVLGDLKEE-----HHFFRRNIILGHRDFERI 57
QY 77 LDAYENKKPFVLYTCRGPSSEAMVGHILPIFTKWLQ---DVENVPLVIQMTDDEKYLW 133
Db 58 VDAIKNNKEFAVSGMPSGK-MHFGHKVVDLLKFKYQYTDNNIPI-----ADLEAYWA 112
QY 134 KDLTDOAGYDAV-ENAKDIIACGPDINKTIFSDLDYMGSSGFYKNVVKI-QKHVTPN 191
Db 113 RNMSPFTKELALNEYIINYIALGLDPEKINVQLSKYQKV-----KDLALILSKRTWS 167
QY 192 QVKGIFGTDSDCTGKISFPALQAAPSFNSFPQIFRDRT--DIQCLIPCAIDQDPTFRM 249
Db 168 EMKAIYGFKGTNIGHVFAPIQVADIL---HPQLDENLSPEPKPVVVPVGVGDQPHIRL 224
QY 250 TRDVAPR---ICYPKALLHSTFPFALQAGTQMSASDPNSISFLTDTAKQIKTKVAKHA 306
Db 225 TRDIANRAKEKFPDPSSTYHRFTWGLLG--KMSSSKPEFAIFLTDDEKIVKKKIFS-A 281
QY 307 FSGGRDTIEHRRQFGG--NCDVDVDSFMYLTFPLEDDKLEQIRKDYTSGLMGTGLX 363
Db 282 KTGGRTELEHKKYGVPECVVYELFLY--HLILDDKELAEIYQKCRSGBELTCGCKKM 339
QY 364 LIEVLQPLIAEHOARKEVTDEIVK 388
Db 340 AYERVVEFLKDLKEKREQAETAVK 364
```

RESULT 12

E69131

tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta H)
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69131
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; J.
; Qiu, D.; Spadator, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct:
A;Reference number: A69000; MUID:98037514; PMID:93711463

A;Accession: E69131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-364 <MTH>
A;Cross-references: UNIPROT:O26352; GB:AE000812; GB:AE000666; NID:g2621298; PIDN:AAB8475.2
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH251
A;Start codon: TTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 18.8%; Score 397.5; DB 2; Length 364;
Best Local Similarity 27.9%; Pred. No. 2.1e-24;
Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14;

15 VDPWTQTSAGKIDYDKLIVRGSSKIDKELINRIERATGQPHPLRRGIFFSHRDNN 74

2 IDPW----GSAK-LEYQDLIENFGVRPF-SEVLDE-----PEPSMLMRRGIIFGHRDYE 50

75 QVLDAYENKKPFVLYTCRGPSSEAMVGHILPIFTKWLQDVENVPLVIQMTDDEKYLW 134

51 RIISAMKKGEDFAVVTGMPPSGR-MHGHKVMVDQLRW-YDRMGAEIPIADIAMEAYSAR 108

135 DLATDOAGYDAVN-AKDIACCFDINK-----TFISDLDYMGSSGFYKNVVK 183

109 GVPFESRRRIAREYTAGYIALGLDEKONHYVOSENLMVEDLAV----- 156

184 IQXHTVFNQVKGIFGTDSDCTGKISFPALQAAPSFNSFPQIFRDRDITDIOCLIPCAIDQ 243

157 LAGKWNFNELRAIVGFTGSTMAMVAPIQVSDILHPQLDELGGPR---PVIVPVGPDQ 213

244 DPFRMTRDVAPRI---GYPKALLHSTFPFALQAGTQMSASDPNSISFLTDTAKQIK 299

214 DPHIRLTRDIAARFDRYGFILPSSTYHRFMGGITGG--KMSNRPKSAIFLSDTPEAE 271

300 TKVNGHAFSGGRDTIEHROFGGNCVDVDSFMYLTFPLE-DDDKLEQIRKDYTSGLMGTG 358

272 AKI-RNAKTGRETLEKQRELGGVPECIYETLLYHMGSDSRLSEIYESCRNGLMCG 330

359 ELKALIEVLQPLIAEHOARKE 381

331 ECKNTAEFIRKPFELSVRKEK 353

RESULT 13

T43806

tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)
C;Species: Encephalitozoon cuniculi
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43806

R;Peyret, P.; Brousseau, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.
Mol. Biol. Evol. 15, 683-689, 1998
A;Title: Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene

A;Reference number: Z22693; MUID:98277683; PMID:9615449

A;Accession: T43806

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

Query Match	17.5%;	Score	370.5;	DB	2;	Length	420;
Best Local Similarity	27.3%;	Pred.	No. 3.9e-22;				
Matches	118;	Conservative	60;	Mismatches	166;	Indels	89;
				Gaps			12;
QY	15	VDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHPFLRGRIFPSHRDMN	74				
Db							
	3	VTPWEVGV-----IDYSKLIEEFGMQPF-SEVLPEID-----NPHILMRRAIGFGRDYW	52				
QY	75	QVLDAVENKKPFYLYTGRGSPSEAMVGHLPITFTKWLQDVENVVPLVIOMTDEKYLWK	134				
Db							
	53	RRIEAMQKEPWAVMGFWPDSG-LPHFGKMTWDEIVHQSGAGKAFV-AIADMEAHSVR	110				
QY	135	DLTLDAQYDAVENAKDIIACGPDINKTFFSDLDYMGSSGIFYKNVV-KIQKHTVFNQV	193				
Db							
	111	GLSWKTRRELGLMYIKSIIALGUREDAVIYFQS-----KSHVKDLAPELSAEVNFSEL	164				
QY	194	KGIFGTFDSDCIKISFPALQAAPSNSPQIFRORTDIOCLIPCAIDODPYFRTRDV	253				
Db							
	165	RAIYGFNSDTSLAKMFVTAIQAAAIL---HPQLSDFGPGKPVVVPVVGADQDPHMLRTDL	221				
QY	254	APRI-----	257				
Db	222	AARISIFSPFVGVGRVRSRKGAEYLSLRDLFEFKKIYEEHMDIFGEABEIERAVRKI	281				
QY	258	-----GYPKPALLHSTFPALQGAQTKMSASDPNSSIELTDTAKQIKTKVKNKHPFSGG	310				
Db							
	282	EVEIGGFAFIPSPSTVHRFTTGLTGG---KMSSSKPSYISLLDPPEGAKKWK-AFTGG	338				
QY	311	RDITIEHRQFGGNCDDVDSFMYLTFPLED--DDKLEQIRKDYTSGAMLTGELKKALIEVLQ	369				

Query Match	16.7%	Score 353;	DB 2;	Length 374;
Best Local Similarity	30.4%;	Pred. No. 8.7e-21;		
Matches 119;	Conservative 70;	Mismatches 165;	Indels 38;	Gaps 17
QY	15	VDPWTQTSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHHFLRGGIFFSHRDWN	74	
DB	8	LDPW----GAVEIKDYDRLRLRTGIRFSEVL--PLLRKAGWESFLMRGIIIGRRDPD	61	
QY	75	QVLDAVENKPFYLYTGRGPSSBAMVGHLPFIPTKWLG-DVFNVPVLVIQMTDDKXYLM	133	
DB	62	KILEAKARGERVAVLTCGFMPGSGK-FHFGHLKTVDLQIYLYQNGFKV--FVAIADAFAV	118	
QY	134	KDLTLDOAYGDAVEN-AKDIIACGFDINKT-FISDLDYMGSSGPFYKVVVKIOGHVTFN	191	
DB	119	RRIGREAVRIAVEEYIANMIALGLDPKOTEFYFQ-----TNRGTPYFLQIQFSKGVTA	174	
QY	192	QVKGIGF-FTDSDICIGKISFPALQAAPSFNSFPQIFRDRDIOCLPICAIDQDQPYFRMT	250	
DB	175	EMEAIIYGLTPAKMNASLT---QAADILHVQLDDEYGGYR---HWVVPVGADQDPHLRLT	227	
QY	251	RDVAPR-----IGYPKPAALLHSTTFPALQAGATKMSASDPNSSIFLTDAKQIKTKVKNHA	306	
DB	228	RDLDARMAGVVELERPASTYHKIQGLDG--RKMSRRPDSITIELTDPPEVARNKLFRA	284	
QY	307	FSGCRDTEIHRQFGGNCV-DVSFMVLTFFLEDKLEQIRKQDYS---GAMLTGELUKK	362	
DB	285	LTCGRATAEQRRLGGVPFVCSVYHMDLYHMLPDDGEVKHI---YTSCRLKILCGECKQ	341	
QY	363	ALIEVLQPLIAEHOARKKEVTDIEIVKFMTPR	394	
DB	342	IAMEKLERFIAEHQSRLKAKTIAWLKVEPPR	373	

Search completed: January 10, 2005, 21:23:46
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:06:08 ; Search time 192 Seconds
(without alignments)
1201.694 Million cell updates/sec

Title: US-09-813-718-10_COPY_71_471

Perfect score: 2116

Sequence: 1 SNHGPRATEABEDFVDPWTV.....VTDEIVKFWTPKLSDFDQ 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2101	99.3	471	1	SYW_HUMAN	P23381 homo sapien
2	2101	99.3	471	2	CADG2335	Cadg2335 homo sapi
3	2028.5	95.9	475	1	SYW_BOVIN	P17248 bos taurus
4	1961.5	92.7	475	1	SYW_RABIT	P23612 oryctolagus
5	1957	92.5	475	2	Q9DC65	Q9dc65 mus musculu
6	1957	92.5	481	2	Q99J58	Q99j58 mus musculu
7	1953	92.3	475	2	Q80Z14	Q80zy4 mus musculu
8	1938	91.6	481	1	SYW_MOUSE	P32921 mus musculu
9	1844	87.1	475	2	Q6NUA2	Q6nu2 xenopus lae
10	1844	87.1	475	2	AAH68695	Aah68695 xenopus l
11	1820	86.0	475	2	Q7ZWT7	Q7zwt7 xenopus lae
12	1734	81.9	379	2	Q6P7B0	Q6p7b0 rattus norv
13	1734	81.9	379	2	AAH61752	Aah61752 rattus no
14	1734	81.9	463	2	Q6PBS3	Q6pbs3 brachydanio
15	1734	81.9	463	2	AAH59603	Aah59603 brachydan
16	1537	72.6	305	2	Q70184	Q70184 cavia porce
17	1439.5	68.0	480	2	Q7Q9D2	Q7q9d2 anopheles g
18	1437.5	67.9	480	2	Q7Q9H6	Q7q9h6 anopheles g
19	1374.5	65.0	420	2	Q9U4Y0	Q9u4y0 drosophila
20	1374.5	65.0	430	2	Q9U4Y1	Q9u4y1 drosophila
21	1370.5	64.8	430	2	Q9VHG2	Q9vhg2 drosophila
22	1323	62.5	417	2	Q9UIR2	Q9uir2 caenorhabdi
23	1304	61.6	438	2	Q6CF80	Q6cfa0 yarrowia li
24	1301	61.5	402	2	Q9SR15	Q9sr15 arabidopsis
25	1210	57.2	395	1	SYW_SCHPO	Q9692 schizosacch
26	1209	57.1	491	2	Q870U0	Q870u0 neurospora
27	1180	55.8	425	2	Q6FQB6	Q6fqb6 candida gla
28	1172	55.4	432	2	Q6CW15	Q6cw15 kluyveromyc
29	1164.5	55.0	421	2	Q6BIL0	Q6bil0 debaryomyc
30	1163	55.0	432	1	SYWC_YEAST	Q12109 saccharomyc
31	1154.5	54.6	426	2	Q75A13	Q75a13 ashbya goss

32 1154.5 54.6 426 2 AAS52037
33 1026 48.5 632 2 Q8IDW3
34 998 47.2 687 2 Q7RB96
35 942 44.5 385 2 Q8SQV5
36 916 43.3 429 2 Q7R0U7
37 910.5 43.0 381 1 SYW_SULTO
38 905 42.8 380 1 SYW_SULSO
39 826.5 39.1 385 1 SYW_PYRFU
40 803 37.9 385 1 SYW_PYRAB
41 796 37.6 386 1 SYW_PYRHO
42 795.5 37.6 490 2 Q9UIF5
43 735 34.7 375 1 SYW_PYRAE
44 701 33.1 377 2 Q74MK6
45 701 33.1 377 2 AAR38970

ALIGNMENTS

RESULT 1

SYW_HUMAN STANDARD; PRT; 471 AA.
AC P23381; P78535; Q9UDL3;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
GN (TrpRS) (IFP53) (hWRS).
DN Name=WARS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92105071; PubMed=1761529;
RA Rubin B.Y., Anderson S.L., Xing L., Powell R.J., Tate W.P.;
RT "Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts.";
RL J. Biol. Chem. 266:24245-24248(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92107982; PubMed=1763065;
RA Fleckner J., Rasmussen H.H., Justesen J.;
RT "Human interferon gamma potentially induces the synthesis of a 55-kDa protein (gamma 2) highly homologous to rabbit peptide chain release factor and bovine tryptophanyl-tRNA synthetase.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:11520-11524(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112058; PubMed=1765274;
RA Erolova L.Y., Sudomoina M.A., Grigorieva A.Y., Zinovieva O.L., Kisselev L.L.;
RT "Cloning and nucleotide sequence of the structural gene encoding for human tryptophanyl-tRNA synthetase.";
RL Gene 109:291-296(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92164636; PubMed=1537332;
RA Buwitt U., Fiohr T., Boettger E.C.;
RT "Molecular cloning and characterization of an interferon induced human cDNA with sequence homology to a mammalian peptide chain release factor.";
RL EMBO J. 11:489-496(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalls D.E.,
RA Smerchek A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [6]
RN MEDLINE=96319994; PubMed=724762;
RX Sokolova I.V., Narovlianskii A.N., Amchenkova A.M., Turpaev K.T.;
RA "Alternative splicing of 5'-terminal exons of the human tryptophanyl-
RT tRNA synthetase gene";
RT Mol. Biol. (Mosk.) 30:319-329 (1996).
RN [7]
RN SEQUENCE OF 1-141 AND 182-471 FROM N.A.
RC TISSUE=Sperm;
RC MEDLINE=93292992; PubMed=7685728;
RX Frolova L.Y., Grigorjeva A.Y., Sudomoina M.A., Kiselev L.L.;
RA "The human gene encoding tryptophanyl-tRNA synthetase: interferon-
RT response elements and exon-intron organization";
RL Gene 128:237-245 (1993).
RN [8]
RN SEQUENCE OF 265-276; 278-296; 299-317 AND 350-365.
RC TISSUE=Keratocytes;
RX MEDLINE=93162043; PubMed=1286667;
RX Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vanderkerckhove J.;
RA "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes";
RL Electrophoresis 13:960-969 (1992).
RN [9]
RN FUNCTION.
RX MEDLINE=92225128; PubMed=1373391;
RX Bange F.-C., Flohr T., Buwitt U., Boettger E.C.;
RA "An interferon-induced protein with release factor activity is a
RT tryptophanyl-tRNA synthetase";
RL FEBS Lett. 300:162-166 (1992).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer.
CC -1- INDUCTION: By interferon gamma.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -1- SIMILARITY: Contains 1 WHEP-TFS domain.
CC -----
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CC -----
CC EMBL; M77804; AAA67324.1; -;
CC EMBL; X59892; CAA42545.1; -;
CC EMBL; M61715; AAA61298.1; -;
CC EMBL; X62570; CAA44450.1; -;
CC EMBL; BC017489; AAA17489.1; -;
CC EMBL; S82905; AAB39381.1; -;
CC EMBL; X67920; CAB94198.1; -;
CC EMBL; X67921; CAB94198.1; JOINED.
CC EMBL; X67922; CAB94198.1; JOINED.
CC EMBL; X67923; CAB94199.1; -;
CC EMBL; X67924; CAB94199.1; JOINED.
CC EMBL; X67925; CAB94199.1; JOINED.

DR EMBL; X67926; CAB94199.1; JOINED.
DR EMBL; X67927; CAB94199.1; JOINED.
DR EMBL; X67928; CAB94199.1; JOINED.
DR PR; A41633; A41706.
DR PDB; 1R6T; X-ray; A/B=1-471.
DR PDB; 1R6U; X-ray; A/B=48-471.
DR PDB; 1ULH; X-ray; A/B=82-471.
DR Aarhus/Ghent-2DPAGE; 3524; IEF.
DR OGP; P23381; -;
DR PHCI-2DPAGE; P23381; -;
DR Genew; HGNC:12729; WARS.
DR MM; 191050; -;
DR GO; GO:0005737; C:Cytoplasm; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0006412; P:protein biosynthesis; TAS.
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; TAS.
DR InterPro; IPR009068; S15/NS1 bind.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR000738; WHEP-TFS.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PF00458; WHEP-TFS; 1.
DR PRINTS; PRO1039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; 1.
DR PROSITE; PS00762; WHEP-TFS; 1.
KW 3D-structure; Aminoacyl-tRNA synthetase; ATP-binding;
KW Direct protein sequencing; Ligase; Protein biosynthesis.
FT DOMAIN 19 64
FT SITE 164 173 "HIGH" region.
FT SITE 349 353 "KMSKS" region.
FT CONFLICT 213 214 SY -> GD (in Ref. 3).
FT CONFLICT 424 424 A -> R (in Ref. 4).
SQ SEQUENCE 471 AA; 53165 MW; E9634444903A0D0 CRC64;
Query Match 99.3%; Score 2101; DB 1; Length 471;
Best Local Similarity 99.5%; Pred. No. 5.4e-160;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SNHGPDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDATAEEDFVDPWTVTQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDMQVLDAYENKKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 120
Db 131 FLRGIFFSHRDMQVLDAYENKKPFYLYTGRGSPSEAMHVGHILPIFTKWLQDVNP 190
Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFFISDLVGMSSGFYKN 180
Db 191 LVIQMTDDEKYLWKDLTLDQAYSAYAVENAKDIIACGPDINKTFFISDLVGMSSGFYKN 250
Qy 181 VKIQKHVTNQVKGIFGFTDSCIGKISPAQAAPSFNSPQIFRDRDTIOCLIPCA 240
Db 251 VKIQKHVTNQVKGIFGFTDSCIGKISPAQAAPSFNSPQIFRDRDTIOCLIPCA 310
Qy 241 IDQDPYFRMTDVAPRIGYKPKALLHSTFFPALQCAQTKMSASDPNSSIFLDTAKQIKT 300
Db 311 IDQDPYFRMTDVAPRIGYKPKALLHSTFFPALQCAQTKMSASDPNSSIFLDTAKQIKT 370
Qy 301 KVNKHAFFSGGRDTIEHRQFGNGCDVDVSPFMYLTFPLEDDDKLBQIRKDYTSGLMTGEL 360
Db 371 KVNKHAFFSGGRDTIEHRQFGNGCDVDVSPFMYLTFPLEDDDKLBQIRKDYTSGLMTGEL 430
Qy 361 KCALEIVQLPLIAHQARRKEVTDEIVKEFWTPKLSFDFQ 401
Db 431 KCALEIVQLPLIAHQARRKEVTDEIVKEFWTPKLSFDFQ 471
RESULT 2
CAD62335
ID CAD62335 PRELIMINARY; PRT; 471 AA.


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AC CAD62335;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Human full-length cDNA clone CS0DM004YH09 of Fetal liver of Homo
DE sapiens (human).
OS Homo sapiens (human).
OG Plasmid pcMVSPORT_6.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Genoscope;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Gueguen M., Sarger C., Labouesse B., Bonnet J.,
RA Labouesse J., Bonnet J.,
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -|- SUBUNIT: Homodimer.
CC -|- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -|- SIMILARITY: Contains 1 WHEP-TRS domain.
CC
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CC
DR EMBL; X53918; CAA37872.1; -
DR EMBL; X52113; CAA36356.1; -
DR PIR; A02779; YWEO.
DR HSP; P07814; IFYD.
DR InterPro; IPR009068; S15/NSI_bind.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR000738; WHEP-TRS.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR Pfam; PF00458; WHEP-TRS; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRfams; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA tRNA LIGASE_I; 1.
DR PROSITE; PS00782; WHEP-TRS; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Direct protein sequencing;
KW Ligase; Protein biosynthesis.
KW DOMAIN 24 69 WHEP-TRS.
FT DOMAIN 1 117 DISPENSABLE TO THE CATALYTIC ACTIVITY.
FT SITE 169 178 "HIGH" region.
FT SITE 353 357 "KMSKS" region.
FT CONFLICT 17 17 L -> M (in Ref. 2).
SQ SEQUENCE 475 AA; 53729 MW; F7E531750137EB32 CRC64;

Query Match 99.3%; Score 2101; DB 2; Length 471;
Best Local Similarity 99.5%; Pred. No. 5.4e-160;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
DB 71 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
QY 61 FLRRGIFFSHRDQVLDAYENKPPFLYTGRCPSSEAMHVGLIPFIPTKWLQDVFNVP 120
DB 131 FLRRGIFFSHRDQVLDAYENKPPFLYTGRCPSSEAMHVGLIPFIPTKWLQDVFNVP 190
QY 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
DB 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 250
QY 181 VVKIQHVTNQVKGIFGFTSDICIGISPAPAOAPSPNSFPQIPRDRDTIQCLIPCA 240
DB 251 VVKIQHVTNQVKGIFGFTSDICIGISPAPAOAPSPNSFPQIPRDRDTIQCLIPCA 310
QY 241 IDQDPYFRMTDVPAPRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFELDTAKQIKT 300
DB 311 IDQDPYFRMTDVPAPRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFELDTAKQIKT 370
QY 301 KVNKHFSGGRDITIEHRQFGNCVDVSPMYLTFFLEDDDKLEQIRKDYTGAMLTGEL 360
DB 371 KVNKHFSGGRDITIEHRQFGNCVDVSPMYLTFFLEDDDKLEQIRKDYTGAMLTGEL 430
QY 361 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDQ 401
DB 431 KKALIEVLQPLIAHQARRKEVTDEIVKEFWTPRKLSFDQ 471

RESULT 3
SYW BOVIN
ID AC P17248;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
GN Name=WARS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
```

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QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIOAAPSFSNSPFIQIRDRDTIOCLIPCA 240
Db 255 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIOAAPSFSNSPFIQIRDRDTIOCLIPCA 314
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAOTKMSADPNSSIFLTDTAKOIKT 300
Db 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAOTKMSADPNSSIFLTDTAKOIKT 374
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360
Db 375 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 434
QY 361 KKALIEVLQPLIAEHQARRKEVTDIVKEFMTPRKLSFDQ 401
Db 435 KKALIEVLQPLIAEHQARRKEVTDIVKEFMTPRKLSFDQ 475

RESULT 4
SYW RABBIT
ID SYW RABBIT STANDARD; PRT; 475 AA.
AC P23612; Q28607;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
DE Name=WARS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90239043; PubMed=2185472;
RA Lee C.C., Craigm W.J., Muzny D.M., Harlow E., Caskey C.T.;
RT "Cloning and expression of a mammalian peptide chain release factor
with sequence similarity to tryptophanyl-tRNA synthetases.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).
[2]
RP REVISIONS TO 169-174 AND 227-228, AND FUNCTION.
RX MEDLINE=94009008; PubMed=8404867;
RA Frolova L.Y., Dalphin M.E., Justesen J., Powell R.J., Drugeon G.,
RA McCaughan K.K., Kiselev L.L., Tate W.P., Haenni A.-L.;
RT "Mammalian polypeptide chain release factor and tryptophanyl-tRNA
synthetase are distinct proteins.";
RL EMBO J. 12:4013-4019(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -1- SIMILARITY: Contains 1 WHEP-TRS domain.
CC -1- CAUTION: Was originally (Ref.1) thought to be a eukaryotic release
factor (ERF).
CC
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CC
CC ENBL; M33460; AAA31246.1; ALT_SEQ.
DR ENBL; U02595; AAB60257.1; -.
DR HSP; P07814; IRYJ.
DR InterPro; IPR009068; S15/NS1_bind.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR014112; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR InterPro; IPR000738; WHEP-TRS.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR Pfam; PF00458; WHEP-TRS; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.

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DR TIGRFAMS; TIGR00233; trpS; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
DR PROSITE; PS00762; WHEP TRS; 1.
KW Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis.
FT DOMAIN 23 68 WHEP-TRS
FT SITE 168 177 "HIGH" region.
FT SITE 353 357 "KMSKS" region.
SQ SEQUENCE 475 AA; 53799 MW; 33BC9E718F45DC4 CRC64;

Query Match 92.7%; Score 1961.5; DB 1; Length 475;
Best Local Similarity 91.5%; Pred No. 8.6e-149;
Matches 367; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 2 NHG-PDATEAEEDFVDPWTQTSSAKGIDYDKLIVRFSGSSKIDKELINRIERATGQRP 60
Db 75 SHGDPEAVDDKEDFVDPWTVRTSSAKGIDYDKLIVFGSSKIDKELVNIERATGQRP 134
QY 61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGFSSEAMHVGHLLPIFTKWLQDVNP 120
Db 135 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGFSSEAMHVGHLLPIFTKWLQDVNP 194
QY 121 LVIQMTDDKYLWKDLTLDQAYGDVAVENAKDIITACGFDINKTFISDLDMGSSGFYKN 180
Db 195 LVQMSDDKYLWKDLTLEQVGYTLENAKDIITACGFDVKNKTFISDLDMGSSGFYKN 254
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIOAAPSFSNSPFIQIRDRDTIOCLIPCA 240
Db 255 VVKIQHVTNQVKGIFGFTSDSCIGKISPAIOAAPSFSNSPFIQIRDRDTIOCLIPCA 314
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAOTKMSADPNSSIFLTDTAKOIKT 300
Db 315 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAOTKMSADPNSSIFLTDTAKOIKT 374
QY 301 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 360
Db 375 KVNKHAFSGGRDTIEHRQFGGNCDDVDSFMYLTFLEDDDKLEQIRKDYTSGLMTGEL 434
QY 361 KKALIEVLQPLIAEHQARRKEVTDIVKEFMTPRKLSFDQ 401
Db 435 KKALIEVLQPLIAEHQARRKEVTDIVKEFMTPRKLSFDQ 475

RESULT 5
Q9DC65
ID Q9DC65 PRELIMINARY; PRT; 475 AA.
AC Q9DC65;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200002C07 product:tryptophanyl-tRNA synthetase, full insert
sequence.
GN Name=Wars;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishigaki T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Adakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK004541; BAB23357.1; -.
DR HSSP; P07814; 1FYJ.
DR MGD; MGI:104630; Wars.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004830; F:tryptophan-tryptophan ligase activity; IEA.
DR GO; GO:0006436; P:tryptophanyl-tryptophan aminoacylation; IEA.
DR InterPro; IPR009068; S15/NS1_bind.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp_cRNA-synt_1b.
DR InterPro; IPR000738; WHEP-TRS.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR Pfam; PF00458; WHEP-TRS; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; tps; 1.
DR PROSITE; PS00178; AA tRNA_LIGASE_I; 1.
DR PROSITE; PS00762; WHEP-TRS; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 475 AA; 53641 MW; C3467FE85521DE4C CRC64;

Query Match 92.58; Score 1957; DB 2; Length 475;
Best Local Similarity 91.58; Pred. No. 2e-148;
Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 NHGDFIFSHRDMNQILDAYENKPFYLYTGRGSSSEAMHGLHLPFTFTKWLQDVFVNPL 61
DB 76 NCSDATKASEDFVDPWTVTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRPHRF 135
QY 62 LRRGIFFSHRDMNQILDAYENKPFYLYTGRGSSSEAMHGLHLPFTFTKWLQDVFVNPL 121

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DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002306; Trp tRNA-synt_1b.
 DR InterPro; IPR000738; WHEP-TRS.
 DR Pfam; PF00579; tRNA-synt_1b; 1.
 DR Pfam; PF00458; WHEP-TRS; 1.
 DR PRINTS; PR01039; TRNASYNTHTRP.
 DR TIGRFAMs; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA TRNA LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP-TRS; 1.
 KW Aminoacyl-tRNA synthetase.
 SQ SEQUENCE 481 AA; 54325 MW; A754E1DDF58E2EF3 CRC64;

Query Match 92.5%; Score 1957; DB 2; Length 481;
 Best Local Similarity 91.5%; Pred. No. 2e-148;
 Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 2 NHGPDATAEEDFVDPWTVOTSSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHHF 61
 DB 76 NCSDATKASEDFVDPWTVOTSSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHF 135

QY 62 LRGGIFSHRDMQVLDAYENKPPFYLYTGRGSPSEAMHGLHPFFFTKWLQDVFNPL 121
 DB 136 LRGGIFSHRDMQVLDAYENKPPFYLYTGRGSPSEAMHGLHPFFFTKWLQDVFNPL 195

QY 122 VIQWTDDEKYLWKDLTLDDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKNV 181
 DB 196 VIQMSDDEKYLWKDLTLLEQAYSIVTENAKDIIACGFDINKTFIFSDLEYMGQSPGFYRNV 255

QY 182 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCAI 241
 DB 256 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAVQAQPSFNSFPKIFRDRDIOCLIPCAI 315

QY 242 DQDPYFMRTRDVAPRIGHPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKTK 301
 DB 376 VNKHAFSGGRDTEEHQFGNCEVDVSFMYLTFLEDDDELEQIRKDYTSGLMTGELK 435

QY 362 KALIEVLQPLIAEHAQARRKEVTDIVKFEFMTPRKLSFDQ 401
 DB 436 KTLIDVLQPLIAEHAQARRKAVTEETVKFEFMTPRQLSFHFQ 475

RESULT 7
 Q80ZY4 PRELIMINARY; PRT; 475 AA.
 AC Q80ZY4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Wars protein.
 GN Name=Wars;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=2338257; PubMed=12477932;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046232; AAH46232.1; -.
 DR HSSP; P07814; IFYJ.
 DR MGD; MGI:104630; Wars.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004830; P:tryptophan-tRNA ligase activity; IEA.
 DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR009068; S15/NS1 bind.
 DR InterPro; IPR002305; tRNA-synt_1b.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR000738; WHEP-TRS.
 DR Pfam; PF00579; tRNA-synt_1b; 1.
 DR Pfam; PF00458; WHEP-TRS; 1.
 DR PRINTS; PR01039; TRNASYNTHTRP.
 DR TIGRFAMs; TIGR00233; trps; 1.
 DR PROSITE; PS00178; AA TRNA LIGASE_I; 1.
 DR PROSITE; PS00762; WHEP-TRS; 1.
 SQ SEQUENCE 475 AA; 53613 MW; D841D8B26973F214 CRC64;

Query Match 92.3%; Score 1953; DB 2; Length 475;
 Best Local Similarity 91.2%; Pred. No. 4.1e-148;
 Matches 365; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 2 NHGPDATAEEDFVDPWTVOTSSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHHF 61
 DB 76 NCSDATKASEDFVDPWTVOTSSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHF 135

QY 62 LRGGIFSHRDMQVLDAYENKPPFYLYTGRGSPSEAMHGLHPFFFTKWLQDVFNPL 121
 DB 136 LRGGIFSHRDMQVLDAYENKPPFYLYTGRGSPSEAMHGLHPFFFTKWLQDVFNPL 195

QY 122 VIQWTDDEKYLWKDLTLDDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFYKNV 181
 DB 196 VIQMSDDEKYLWKDLTLLEQAYSIVTENAKDIIACGFDINKTFIFSDLEYMGQSPGFYRNV 255

QY 182 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAIQAPSFNSFPQIFRDRDIOCLIPCAI 241
 DB 256 VKIQKHVTFNQVKGIFGTFDSDCIGKISFPAVQAQPSFNSFPKIFRDRDIOCLIPCAI 315

QY 242 DQDPYFMRTRDVAPRIGHPKALLHSTFFPALQAGTQMSASDPNSSIFLDTAKQIKTK 301
 DB 376 VNKHAFSGGRDTEEHQFGNCEVDVSFMYLTFLEDDDELEQIRKDYTSGLMTGELK 435

QY 362 KALIEVLQPLIAEHAQARRKEVTDIVKFEFMTPRKLSFDQ 401
 DB 436 KTLIDVLQPLIAEHAQARRKAVTEETVKFEFMTPRQLSFHFQ 475

RESULT 8
 Q80ZY4 PRELIMINARY; PRT; 481 AA.
 ID SYM MOUSE
 AC P32921;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)

Query Match 81.9%; Score 1734; DB 2; Length 379;
Best Local Similarity 92.2%; Pred. No. 1.2e-130;
Matches 321; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

Matches 321; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 1 SNHGPDATAEEDFVDPTWVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP 60
 DB 30 SNGDPDATKASEDFVDPTWVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP 89
 QY 61 FLRRGIFFSHRDMMQVLDAYENKPFYLYTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 120
 DB 90 FLRRGIFFSHRDMMQVLDAYENKPFYLYTGRGSSSEAMHVGHLIPFIPTKWLQDVNP 149
 QY 121 LVQMTDDEKYLWKDLTDOAYGDAVENAKDIIACGFDINKTFIFSDLDYMGSSGFGYKN 180
 DB 150 LVQMSDDEKYLWKDLTLEQAYSVTVENAKDIIACGFDVNTKTFIFSDLEYMGSSGFGYKN 209
 QY 181 VKIQKHVTNQNKGIFGFTSDSCIGKISPAIOAAPSFSNPFQIIFRDRDIOCLIPCA 240
 DB 210 VKIQKHVTNQNKGIFGFTSDSCIGKISPAIOAAPSFSNPFQIIFRDRDIOCLIPCA 269
 QY 241 IDQDPYFRMTRDVAPRIGYPKPKALLHSTFFPALQGAOTKMSASDPNSSIFLDTAKQIKT 300
 DB 270 IDQDPYFRMTRDVAPRIGYPKPKALLHSTFFPALQGAOTKMSASDPNSSIFLDTAKQIKS 329
 QY 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVVSFMYLTFPLEDDDKLEQIRK 348
 DB 330 KVNKHAFFSGGRDTIEHRQFGGNCVDVVSFMYLTFPLEDDDKLEQIRK 377

RESULT 13

AAH61752
 ID AAH61752 PRELIMINARY; PRT; 379 AA.
 AC Q6PBS3
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC061752; AAH61752.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 379 AA; 42880 MW; B9CDB2248780C2E1 CRC64;

Query Match 81.9%; Score 1734; DB 2; Length 379;
 Best Local Similarity 92.2%; Pred. No. 1.2e-130;

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Job time : 196 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:16:34 ; Search time 40 Seconds
(without alignments)
664.838 Million cell updates/sec

Title: US-09-813-718-10_COPY_71_471

Perfect score: 2116
Sequence: 1 SNHGPPATEAEEDFVDPWT.....VTDEIVKEFTRPKUSFDFQ 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/iaa/PCtUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	774.5	36.6	210	4	US-09-270-767-61162
5	684.5	32.3	255	4	US-09-248-796A-19803
6	550	26.0	213	4	US-09-248-796A-19802
7	195	9.2	338	4	US-09-328-352-4201
8	186	8.8	348	4	US-09-107-532A-5765
9	185.5	8.8	341	3	US-08-928-100-2
10	185.5	8.8	341	3	US-09-492-581-2
11	185.5	8.8	341	4	US-09-425-666-2
12	183.5	8.7	341	4	US-09-563-110-4392
13	174	8.2	335	4	US-09-134-000C-5784
14	164.5	7.8	409	2	US-08-743-130A-39
15	162.5	7.7	409	2	US-08-743-130A-2
16	157.5	7.4	385	4	US-09-489-039A-8660
17	152	7.2	344	4	US-09-198-452A-857
18	141	6.7	346	4	US-09-248-796A-18205
19	132.5	6.3	388	2	US-08-705-868-4
20	132.5	6.3	388	3	US-09-123-615-4
21	123	5.8	356	4	US-09-543-681A-4257
22	118	5.6	349	4	US-09-543-681A-6769
23	118	5.6	426	4	US-09-107-532A-4046
24	113.5	5.4	418	3	US-08-855-910-11
25	113.5	5.4	433	4	US-09-134-000C-3686
26	109	5.2	377	3	US-09-352-990-28
27	108	5.1	197	2	US-08-923-867-2

28	108	5.1	197	3	US-08-928-100-4	Sequence 4, Appli
29	108	5.1	197	3	US-09-183-134-2	Sequence 2, Appli
30	108	5.1	197	3	US-09-492-581-4	Sequence 4, Appli
31	108	5.1	197	4	US-09-425-666-4	Sequence 4, Appli
32	106	5.0	404	4	US-09-248-796A-17676	Sequence 17676, A
33	104.5	4.9	370	2	US-08-415-593-45	Sequence 45, Appl
34	100.5	4.7	421	4	US-09-710-279-1820	Sequence 1820, Ap
35	100.5	4.7	427	3	US-09-134-001C-5141	Sequence 5141, Ap
36	97.5	4.6	335	4	US-09-489-039A-10919	Sequence 10919, A
37	96.5	4.6	374	4	US-09-248-796A-15744	Sequence 15744, A
38	95	4.5	418	3	US-08-844-054-2	Sequence 2, Appli
39	95	4.5	418	3	US-09-347-333-2	Sequence 2, Appli
40	95	4.5	418	4	US-09-583-110-4220	Sequence 4220, Ap
41	95	4.5	459	4	US-09-710-279-1246	Sequence 1246, Ap
42	95	4.5	459	4	US-09-710-279-2554	Sequence 2554, Ap
43	95	4.5	464	3	US-09-134-001C-4701	Sequence 4701, Ap
44	94.5	4.5	877	2	US-08-907-166-8	Sequence 8, Appli
45	94.5	4.5	877	4	US-09-391-340-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-919-039-163
; Sequence 163, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 163
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2705515CD1
US-09-919-039-163

Query Match		99.3%	Score 2101;	DB 4;	Length 471;
Best Local Similarity		99.5%	Pred. No. 3e-227;		
Matches 399;		Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	SNHGPPATEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP	60		
Db	71	SNHGPPATEAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP	130		
Qy	61	FLRRGIFFSHRDQVLDAYENKKPYLYTGRGSPSEAMHVGHLIPFIFTKWLQDVNPV	120		
Db	131	FLRRGIFFSHRDQVLDAYENKKPYLYTGRGSPSEAMHVGHLIPFIFTKWLQDVNPV	190		
Qy	121	LVIQMTDDEKYLKDLTDQAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSGGYKN	180		
Db	191	LVIQMTDDEKYLKDLTDQAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSGGYKN	250		
Qy	181	VVKIQHVTNQVKGIFGFTDSCIGKISPPALQAPSPFNSPPOIFRDRDTDQCLIPCA	240		
Db	251	VVKIQHVTNQVKGIFGFTDSCIGKISPPALQAPSPFNSPPOIFRDRDTDQCLIPCA	310		
Qy	241	IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFLDTAKQIKT	300		
Db	311	IDQDPYFRMTRDVAIRIGYKPKALLHSTFFPALQGAQTKMSADPNSSIFLDTAKQIKT	370		
Qy	301	KVNKHAFFSGGRDIEBHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	360		
Db	371	KVNKHAFFSGGRDIEBHRQFGGNCVDVVSFMYLTFLEDDDKLEQIRKDYTSGAMLTGEL	430		

QY 361 KKALIEVLQPLIAHQARRKEVTDIIVKEFWTPRKLSFDFQ 401
 Db 431 KKALIEVLQPLIAHQARRKEVTDIIVKEFWTPRKLSFDFQ 471

RESULT 2

US-09-270-767-45650
 ; Sequence 45650, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45650

; LENGTH: 401

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-45650

Query Match 61.0%; Score 1290.5; DB 4; Length 401;

Best Local Similarity 67.4%; Pred. No. 3.6e-136;

Matches 240; Conservative 51; Mismatches 64; Indels 1; Gaps 1;

QY 7 ATAEEDFVDPWTVQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRPHPFLRGI 66

Db 46 ATATEDVDPWNVASSNDAGVDYDKLIVRGSSKIDKELIARPEXITGKPAHHFIRKGM 105

QY 67 FFSHRDNQVLDAYENKPPFLYTGGRPSSEAMVGHILIPFIETKWLQDVFNVLQMT 126

Db 106 FFSHRDLHTLTREOQKPPFLYTGGRPSGSLVGHVLPFIMTKLQETFDVPLVLT 165

QY 127 DDEKYLWDLTDQAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSGFYKNVQIK 186

Db 166 DDEKTLWDLKVEDAKILGRENAKDIIAIGFDVNTKTFNNLEFVGKCPAQYQNIIRIQ 225

QY 187 HVTFNQVKGIFGFTSDSCIGKISPAIAQAPSFNSFPQIPRDRDTIQCLIPCAIDQDPY 246

Db 226 CVTFNQVKGIFGSDSDIIGKIGFPAQAAPASSTFFFIQGNR-KVHCLIPCAIDQDPY 284

QY 247 FRMTRDVAPRIGYPKPAIHLSTFFPALQCAQTKMSASDPNSSIILTTAKQIKTKVKA 306

Db 285 FRMTRDVAPRIGYPKPAIHLSTFFPALQCAQTKMSASDPNSSIILTTAKQIKTKVKA 344

QY 307 FSGGRDTIEHRQFGGNCVDVSPWLTFFLEDDDKLEQIRKDYTSGLMTGLKK 362

Db 345 FSGGRVTVEHRKLGVPVDVSYQLLKFLEDDAKLEEVRAVSKGEMLTGEIKK 400

RESULT 3

US-08-876-885-26

; Sequence 26, Application US/08876885

; Patent No. 6174713

; GENERAL INFORMATION:

; APPLICANT: Shen, Xiaoyu

; APPLICANT: Homan, Fariba

; TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-TRNA

; TITLE OF INVENTION: SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/876,885

APPLICANT NUMBER: 16-JUN-1997

FILING DATE: 16-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: CPI97-02

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 861-6240

TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 424 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-876-885-26

Query Match 57.6%; Score 1218.5; DB 3; Length 424;

Best Local Similarity 57.1%; Pred. No. 5e-128;

Matches 226; Conservative 71; Mismatches 92; Indels 7; Gaps 3;

QY 8 TEAEEDFVDPWTVQ----TSSAKGIDYDKLIVRGSSKIDKELINRIERATGQRPHPFLR 63

Db 13 TESEOKITPWEVAGAVDVGKSGIDYDKLISQFGTKHITTEILERPKQVTGEPHPFLK 72

QY 64 RGIFFFHRDNQVLDAYENKPPFLYTGGRPSSEAMVGHILIPFIETKWLQDVFNVLVI 123

Db 73 RGVFFSQRLDLRLDLYEHGEPEFLYTGGRPSSDSMHLGHVWFFIFTKWLQEVDFVLVI 132

QY 124 QMTDDKYLWK-DLTDQAYGDAVENAKDIIACGPDINKTIFISDLDYMGSSGFYKNVV 182

Db 133 ELTDDEKFLFKHQLITDDVKGFAAENAKDIIAVGFNPENTFIFSDLYMG--GAFYENVV 190

QY 183 KIQKHTFNQVKGIFGFTSDSCIGKISPAIAQAPSFNSFPQIPRDRDTIQCLIPCAID 242

Db 191 RTGRQITTSKAVAFGFTSDSCIGKIHFAISQIATAPPSFPDVLGLPPTKCLIPCAID 250

QY 243 QDFYFRMTRDVAPRIGYPKPAIHLSTFFPALQCAQTKMSASDPNSSIILTTAKQIKTV 302

Db 251 QDFYFRMTRDVAPRIGYPKPAIHLSTFFPALQCAQTKMSASDPNSSIILTTAKQIKTV 310

QY 303 NKHAFSGGRDTIEHRQFGGNCVDVSPWLTFFLEDDDKLEQIRKDYTSGLMTGLKK 362

Db 311 NKVAFSGGRATAEHRELGNPEVDVAFQYLSFFSYDDEKLAQLEQGYRKGELSGEMKK 370

QY 363 ALTEVLQPLIAHQARRKEVTDIIVKEFWTPRKLSF 398

Db 371 ECITVLQEFVSAYOERRSKVDVQVVEKFMKPKLVF 406

RESULT 4

US-09-270-767-61162

; Sequence 61162, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 61162

; LENGTH: 210

; TYPE: PRT

; ORGANISM: *Drosophila melanogaster*

RESULT 6
US-09-248-796A-19802
; Sequence 19802, Application US/09248796A
; Patent NO. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

Query Match	9.2%;	Score 195;	DB 4;	Length 338;
Best Local Similarity	25.9%;	Pred. No. 5.1e-13;		
Matches	84;	Conservative	56;	Mismatches 138; Indels 46; Gaps 13;
Qy	82	NKPFYLLTGRGSSSEAMHVGHLPIPTFTK-WLQDVENVPLVI-----QMTDDEKYLWKDL	136	
Db	6	DQRPILL-TGDRPTGQ-LHLGHFVGLSRVGLQDSHHQHLLLADAQALTDNAD-----	57	
Qy	137	TLDAQYGDVAVENAKDIIACGFDINKTFIF--SLDYNGMSGSGFYKN---VVKIQKHVTFN	191	
Db	58	NPQKVRNIIIEVALDYLAAGIDPTKTTICVQSCULPALNELTMLYLFNFTVARLERNPTIK	117	
Qy	192	QVKGIQFETSDCIGKISFPAIQAAPSFNSFPQIPRDRTDIOC-LIIPCAIDQDPYFRMT	250	
Db	118	SETQMRGFERDIPAGFLCYIPAQA-----DITAFKATVPVGSVDQIPMEIQT	165	
Qy	251	RDVAPRITGYP-----KPLLHSTFFPALQGAQTQNSASDPNSSIFLTDTAQIKTK	301	
Db	166	NEIVRYNROIQDGLLPECKALLSNMARLPGFDG-KAKMSKSLGN-TIVLNASDKDKKKA	223	

QY 302 VNKHPSGGRTDIEHROFGNCDVDSEMYLTFELEDKLRQIRKDYTSGLMGTGLK 361
Db 224 VNAMYTDPNHLRIEDPGQVEGN-----IVFYLDADFDPNKEEVBELKAHYRGGGLGDTVK 279
QY 362 KALIEVLOPLIAHQARKKEVTDE 385
Db 280 KRLEGVLKELITPIRERREBLAKD 303

RESULT 8
US-09-107-532A-5765
; Sequence 5765, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5765:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...348
; SEQUENCE DESCRIPTION: SEQ ID NO: 5765:
US-09-107-532A-5765

Query Match 8.8%; Score 186; DB 4; Length 348;
Best Local Similarity 24.9%; Pred. No. 5.5e-12;
Matches 82; Conservative 57; Mismatches 120; Indels 70; Gaps 14;

QY 88 LYTGRPSSEAMHVGHLIPFFITKWLQDVFNVPVLIQMTDDEKYLWKDLTLDQAYDAVE 147
Db 17 ILTGDRPTGK-LHLGHYVGS�KTR-----VAMQADENQOLFVMIADMQALTDNAK 65
QY 148 N-----AKDIIACGFDINKT--FIFSDLDYMGMSGFYKNVY---KIQKHVT-- 189
Db 66 NPEKVSSNVQLVADYLAUGLDPKATFLFIQSIPELAELTWYLYLVSVGRVRNPVTK 125

QY 190 --FNQVKGIFGFTSDSCIGKISFPAIQAAPSFNSFPQIFRDRTDIQC-LIPCAIDQDPY 246
Db 126 TEIEQKK---FGESVPTGFFIYVPVQA-----DITAFKANLVPGSDQKPM 169
QY 247 FRMTDD-----VAPRIGYKPKALLHSTFFPALQGAQTMSASDPSNSSFILTD 293
Db 170 LEQTOEIVQSFNHYTYGEVLVEPKGVFPKGMGR---LPGIDG-NGKMSKSLGN-GIYISD 224
QY 294 TAKQIKTKVKNKHAFFSGGRDTIEHRQFGNCDVDSEMYLTFELEDKLRQIRKDYTSG 353
Db 225 PADVLQKKV----MSMYTDPNHHVQDPQGVGNMVFYLDVFGTDKEAIEEMKAHYRRG 280
QY 354 AMLTGELKALIEVLOPLIAHQARKKEV 382
Db 281 GLGDVKIKRYLIDVLEAEFAPIRARREEL 309

RESULT 9
US-08-928-100-2
; Sequence 2, Application US/08928100
; Patent No. 6046174
; GENERAL INFORMATION:
; APPLICANT: Gentry, Danile
; APPLICANT: Greenwood, Claire
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6046174el trps
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,100
; FILING DATE: 12-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9619072.3
; FILING DATE: 12-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31624-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 341 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-928-100-2

Query Match 8.8%; Score 185.5; DB 3; Length 341;
Best Local Similarity 24.0%; Pred. No. 6.1e-12;
Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

QY 84 KPFFLYTGRPSSEAMHVGHLIPFFITKWLQDVFNVPVLIQMTDDEKY-LWKDLTLDQAY 142
Db 3 KPILL-TGDRPTGK-LHGHYVGS�KTR-----VLLQEDKYDMFVFLADQAL 49
QY 143 GDAVEN-----AKDIIACGFDINKTFF--SDLDYMGMSGFYKNVY---KIQK 186


```

; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,130A
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CP195-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 409 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-743-130A-2

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Query Match	7.7%	Score 162.5;	DB 2;	Length 409;
Best Local Similarity	20.7%;	Pred. No. 3.2e-09;		
Matches	78;	Conservative	59;	Mismatches 132;
			Indels 107;	Gaps 16;
Qy	76	VLDAYENK-kppvlytgrgssbamvghlippi-	-----FTKMLQDV-----F	117
Db	27	IKDVKENRPVKIYWGTAFTGXP-HCGYFVPMIKLAHFLKAGCEVTVLLADLHAFLDNM	85	
Qy	118	NVPLVIMTDDKEYLWKMDLTDQAYGDAVENAKDIIACGDFDKTIFPSLDLYNMGSSGF	177	
Db	86	KAPLEVVKYRAKYEFVFKAILKINSNPIERLKFVVGSSYQKGDDYV---MDLFKLSNIV	142	
Qy	178	YKNVVK-----IOKHYTFNVOKGIFGFTDSDCIGKISFPAIQAAPSFSNFPQIFRQRTD	232	
Db	143	SQNDAKRAGADVVKQVANPLSLGI-----YPLMQA-----IDEEHLG	180	
Qy	233	IOCLIPCAIDQDPYFRMTRDVAPRIGYPKALLHSTFFPALQAGATKMSASDPNSSIFLT	292	
Db	181	VDAQFG-GVDORKIFVLABENLPSIGYKRAHLMNPMVPGI-GGGKMSASDPNSKIDII	238	
Qy	293	DTAKQIKTKNKHAFSGG--RDT-----IEEHRQCGGN	323	
Db	239	EEPKVKKCKVNSAYCAPGELKDNGLIAFIYVITQPIAELKTGVEGAPKLDIDREPKYGG-	297	
Qy	324	CDVDVGFMYLTFLEDDDKLEQIRKDYTSAMLITGELKKALI-----EVLOPLIAEHAQRR	379	
Db	298	---PLSY-----DSIEQLKADFVQDKLAPPDLKLGVDKINELLAPIRAEFESS-	343	
Qy	380	KEVTDEIVKEFMTPRK	395	
Db	344	-----EEFOVAQK	351	

Search completed: January 10, 2005, 21:24:32
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 21:23:09 ; Search time 145 Seconds
(without alignments)
997.166 Million cell updates/sec

Title: US-09-813-718-10_COPY_71_471

Perfect score: 2116
Sequence: 1 SNHGPDATAEEDFVDPWT.....VTDEIVKFRTPRKLSDFDQ 401

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1603904 seqs, 360571292 residues

Total number of hits satisfying chosen parameters: 1603904

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	401	14	US-10-080-839-13
2	2116	100.0	415	9	US-09-813-718-14
3	2116	100.0	415	14	US-10-080-839-5
4	2116	100.0	415	15	US-10-240-532-14
5	2116	100.0	415	16	US-10-240-527A-14
6	2116	100.0	437	9	US-09-813-718-12
7	2116	100.0	437	14	US-10-080-839-3
8	2116	100.0	437	15	US-10-240-532-12
9	2116	100.0	437	16	US-10-240-527A-12
10	2116	100.0	471	14	US-10-126-467B-2
11	2116	100.0	471	14	US-10-295-027-1234
12	2116	100.0	471	16	US-10-755-889-250
13	2116	100.0	471	17	US-10-370-715B-250

14	2116	100.0	484	9	US-09-813-718-10
15	2116	100.0	484	14	US-10-080-839-1
16	2116	100.0	484	15	US-10-240-532-10
17	2116	100.0	484	16	US-10-240-527A-10
18	2101	99.3	471	10	US-09-919-039-163
19	2101	99.3	471	14	US-10-247-671-166
20	2101	99.3	471	16	US-10-408-765A-1235
21	2101	99.3	471	17	US-10-733-969A-62
22	2101	99.3	475	9	US-09-925-302-558
23	2101	99.3	475	10	US-09-925-302-558
24	1988	94.0	378	14	US-10-080-839-12
25	1988	94.0	378	14	US-09-813-718-16
26	1988	94.0	382	9	US-09-813-718-16
27	1988	94.0	382	14	US-10-080-839-7
28	1988	94.0	392	15	US-10-240-532-16
29	1988	94.0	392	16	US-10-240-527A-16
30	1988	94.0	392	17	US-10-628-783-2
31	1938	91.6	475	14	US-10-205-219-65
32	1326.5	62.7	408	16	US-10-437-963-120838
33	1326	62.7	410	15	US-10-424-599-146807
34	1302	61.5	429	15	US-10-425-114-58867
35	1200.5	56.7	424	14	US-10-032-585-7632
36	1168.5	55.2	519	17	US-10-425-115-347839
37	1125	53.2	433	14	US-10-128-714-8545
38	1107.5	52.3	456	15	US-10-320-797-3204
39	831	39.3	173	9	US-09-925-302-855
40	831	39.3	173	10	US-09-925-302-855
41	710.5	33.6	234	16	US-10-767-701-43019
42	704.5	33.3	324	16	US-10-437-963-108176
43	645	30.5	195	17	US-10-425-115-298233
44	604.5	28.6	192	17	US-10-425-115-347838
45	414.5	19.6	179	14	US-10-128-714-3545
	398	18.8	137	16	US-10-437-963-145795

ALIGNMENTS

RESULT 1

US-10-080-839-13
; Sequence 13, Application US/10080839
; Publication No. US20030017564A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakaue, Keisuke
; APPLICANT: Friedlander, Martin
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
; FILE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
; FILE REFERENCE: TSRI-813.1
; CURRENT APPLICATION NUMBER: US/10/080, 839
; PRIOR FILING DATE: 2002-02-22
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-839-13

Query Match	100.0%	Score	2116	DB	14	Length	401
Best Local Similarity	100.0%	Pred. No.	3.9e-194				
Matches	401	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	SNHGPDATAEEDFVDPWTVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP	PHH	60			
Db	1	SNHGPDATAEEDFVDPWTVTQTSAGIDYDKLIVRGSSKIDKELINRIERATGQRP	PHH	60			
Qy	61	FLRRGIFFSHRDNNQVLDAYENKKPFYLYTGRGSSSAMVGHILPIFTKWLQDVNP	V	120			
Db	61	FLRRGIFFSHRDNNQVLDAYENKKPFYLYTGRGSSSAMVGHILPIFTKWLQDVNP	V	120			
Qy	121	LVIQMTDDEKYLWKDLTLDQAYGDVAKDIACGFDINKTFTFSDLDYMGSSGFYKN		180			

Db 121 LVQMDDDEKYLWKDLTLDOAYGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
Db 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
QY 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
Db 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
RESULT 2
US-09-813-718-14
; Sequence 14, Application US/09813718
; Publication No. US2002018266A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini Trprs in pET20B
US-09-813-718-14
Query Match 100.0%; Score 2116; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
QY 61 FLRRGIFFSHRDMNQVLDAYENKPPFLYTGRGSPSEAMHVGHLPFIETKWLQDVFNVP 120
Db 62 FLRRGIFFSHRDMNQVLDAYENKPPFLYTGRGSPSEAMHVGHLPFIETKWLQDVFNVP 121
QY 121 LVQMDDDEKYLWKDLTLDOAYGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVQMDDDEKYLWKDLTLDOAYGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 181
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 182 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 241
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 301
QY 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 361
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401

Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 402
RESULT 3
US-10-080-839-5
; Sequence 5, Application US/10080839
; Publication No. US20030017564A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; APPLICANT: Friedlander, Martin
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
; FILE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
; FILE REFERENCE: TSRI-813.1
; CURRENT APPLICATION NUMBER: US/10/080,839
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,951
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cleavage Product T1 of recombinant human Trprs
US-10-080-839-5
Query Match 100.0%; Score 2116; DB 14; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPMTVTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
QY 61 FLRRGIFFSHRDMNQVLDAYENKPPFLYTGRGSPSEAMHVGHLPFIETKWLQDVFNVP 120
Db 62 FLRRGIFFSHRDMNQVLDAYENKPPFLYTGRGSPSEAMHVGHLPFIETKWLQDVFNVP 121
QY 121 LVQMDDDEKYLWKDLTLDOAYGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVQMDDDEKYLWKDLTLDOAYGDAVENAKDIACGFDINKTFIFSDLDYMGSSGFYKN 181
QY 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 240
Db 182 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTIQCLIPCA 241
QY 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 301
QY 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPFMYLTFLEDDDDKLEQIRKDYTSGLMTGEL 361
QY 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 401
Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWMPTRKLSFDFQ 402
RESULT 4
US-10-240-532-14
; Sequence 14, Application US/10240532
; Publication No. US20040009163A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.1
; CURRENT APPLICATION NUMBER: US/10/240,532
; CURRENT FILING DATE: 2002-09-30

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; PRIOR APPLICATION NUMBER: PCT/US01/08975
; PRIOR APPLICATION NUMBER: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR APPLICATION NUMBER: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini Trprs in pET20B
US-10-240-532-14

Query Match      100.0%; Score 2116; DB 15; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 120
Db 62 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 121
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 122 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 181
Qy 181 VKIQKHVTNQVKGIFGFTSDCIKISPPAIQAAPSFNSFPQIPRDRTDIOCLIPCA 240
Db 182 VKIQKHVTNQVKGIFGFTSDCIKISPPAIQAAPSFNSFPQIPRDRTDIOCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 301
Qy 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDDKLEQIRKDYTSGAMLTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDDKLEQIRKDYTSGAMLTGEL 361
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 402

RESULT 6
US-09-813-718-12
; Sequence 12, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human mini
; OTHER INFORMATION: Trprs in pET20B
US-09-813-718-12

Query Match      100.0%; Score 2116; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 24 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 83
Qy 61 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 120
Db 84 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 143
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 203
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; PRIOR APPLICATION NUMBER: PCT/US01/08975
; PRIOR APPLICATION NUMBER: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR APPLICATION NUMBER: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: supermini Trprs in pET20B
US-10-240-532-14

Query Match      100.0%; Score 2116; DB 15; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 2 SNHGPDTEAEEDFVDPWTVQTSAGKIDYDKLIVRFGSSKIDKELINRIERATGQRP 61
Qy 61 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 120
Db 62 FLRGIFFSHRDMNQVLDAYENKKPFYLYTGRGSSSEAMHVHGLIPIFTKWLQDVNP 121
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 180
Db 122 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTTFISDLDYMGSSGFYKN 181
Qy 181 VKIQKHVTNQVKGIFGFTSDCIKISPPAIQAAPSFNSFPQIPRDRTDIOCLIPCA 240
Db 182 VKIQKHVTNQVKGIFGFTSDCIKISPPAIQAAPSFNSFPQIPRDRTDIOCLIPCA 241
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 300
Db 242 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALQGAQTMSASDPNSSIELTDTAKQIKT 301
Qy 301 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDDKLEQIRKDYTSGAMLTGEL 360
Db 302 KVNKHAFFSGGRDTIEHRQFGGNCVDVSPMYLTFPLEDDDDKLEQIRKDYTSGAMLTGEL 361
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 362 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 402

RESULT 5
US-10-240-527A-14
; Sequence 14, Application US/10240527A
; Publication No. US20040152079A1
; GENERAL INFORMATION:
; APPLICANT: SCHIMMEL, Paul
; APPLICANT: WAKASUGI, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
; FILE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.2
; CURRENT APPLICATION NUMBER: US/10/240,527A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/08966
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human supermini Trprs in pET20B
US-10-240-527A-14
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181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 240
Db
204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 263
Qy
241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 300
Db
264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 323
Qy
301 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
Db
324 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383
Qy
361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
Db
384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 424

RESULT 7

US-10-080-839-3
; Sequence 3, Application US/10080839
; Publication No. US20030017564A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; APPLICANT: Friedlander, Martin
; TITLE OF INVENTION: Trypophanyl-tRNA Synthetase Derived
; TITLE OF INVENTION: Polypeptides Useful For The Regulation of Angiogenesis
; FILE REFERENCE: TSRI-813.1
; CURRENT APPLICATION NUMBER: US/10/080,839
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,951
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human mini TrpRS in pET20B
US-10-080-839-3

Query Match 100.0%; Score 2116; DB 14; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 24 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83
Qy 61 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLQDVFNVP 120
Db 84 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLQDVFNVP 143
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 203
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 240
Db 204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 263
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 300
Db 264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 323
Qy 301 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
Db 324 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
Db 384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 424

RESULT 8

US-10-240-532-12
; Sequence 12, Application US/10240532
; Publication No. US20040009163A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; TITLE OF INVENTION: The Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.1
; CURRENT APPLICATION NUMBER: US/10/240,532
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/08975
; PRIOR APPLICATION NUMBER: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR APPLICATION NUMBER: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human mini
; OTHER INFORMATION: TrpRS in pET20B
US-10-240-532-12

Query Match 100.0%; Score 2116; DB 15; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 24 SNHGPDATAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83
Qy 61 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLQDVFNVP 120
Db 84 FLRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLQDVFNVP 143
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 180
Db 144 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTIFSDLDYMGSSGFYKN 203
Qy 181 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 240
Db 204 VVKIQHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSFPQIFRDRDTDIQCLIPCA 263
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 300
Db 264 IDQDPYFRMTRDVAPRIGYKPKALLHSTFPALOGAQTQKMSASDPNSSIFLDTAKQIKT 323
Qy 301 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 360
Db 324 KVNKHAFSGGRDITIEHRQFGGNCVDVSPMYLTFPLEDDDKLEQIRKDYTSGLMTGEL 383
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
Db 384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 424

RESULT 9

US-10-240-527A-12
; Sequence 12, Application US/10240527A
; Publication No. US20040152079A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Keisuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
; TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
; FILE REFERENCE: TSRI 720.2
; CURRENT APPLICATION NUMBER: US/10/240,527A

; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/08966
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/193,471
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human mini TrpRS in pET20B
US-10-240-527A-12

Query Match 100.0%; Score 2116; DB 16; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEAEEDFVDPTWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 24 SNHGPDATAEAEEDFVDPTWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 83
Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSAMHVGHLIPFIPTKWLQDVFNVP 120
Db 84 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSAMHVGHLIPFIPTKWLQDVFNVP 143
Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFPSLDYMGSSGGFYKN 180
Db 144 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFPSLDYMGSSGGFYKN 203
Qy 181 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 204 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 263
Qy 241 IDQDPYFRMTRDVAPRIGYKPKPALLHSTFFPALQGAQTQKMSASDPNSSIFLTDTAKQIKT 300
Db 264 IDQDPYFRMTRDVAPRIGYKPKPALLHSTFFPALQGAQTQKMSASDPNSSIFLTDTAKQIKT 323
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVDSFMYLTFPLEDDDKLEQIRKDYTSGAMLGTGEL 360
Db 324 KVNKHAFFSGGRDITIEHRQFGGNCDDVDSFMYLTFPLEDDDKLEQIRKDYTSGAMLGTGEL 383
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
Db 384 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 424

RESULT 10
US-10-126-467B-2
; Sequence 2, Application US/10126467B
; Publication No. US2003005979A1
; GENERAL INFORMATION:
; APPLICANT: Paley, Elena
; TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
; FILE REFERENCE: PALL-111
; CURRENT APPLICATION NUMBER: US/10/126,467B
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,980
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/513,895
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/384,869
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-126-467B-2

Query Match 100.0%; Score 2116; DB 14; Length 471;

Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEAEEDFVDPTWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDATAEAEEDFVDPTWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSAMHVGHLIPFIPTKWLQDVFNVP 120
Db 131 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSPSSAMHVGHLIPFIPTKWLQDVFNVP 190
Qy 121 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFPSLDYMGSSGGFYKN 180
Db 191 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTIFPSLDYMGSSGGFYKN 250
Qy 181 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 310
Qy 241 IDQDPYFRMTRDVAPRIGYKPKPALLHSTFFPALQGAQTQKMSASDPNSSIFLTDTAKQIKT 300
Db 311 IDQDPYFRMTRDVAPRIGYKPKPALLHSTFFPALQGAQTQKMSASDPNSSIFLTDTAKQIKT 370
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVDSFMYLTFPLEDDDKLEQIRKDYTSGAMLGTGEL 360
Db 371 KVNKHAFFSGGRDITIEHRQFGGNCDDVDSFMYLTFPLEDDDKLEQIRKDYTSGAMLGTGEL 430
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFWTPRKLSFDFQ 471

RESULT 11
US-10-295-027-1234
; Sequence 1234, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1234
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1234

Query Match      100.0%; Score 2116; DB 14; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVNP 120
Db 131 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVNP 190
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFFSDLDYMGSSGFYKN 180
Db 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFFSDLDYMGSSGFYKN 250
Qy 181 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 310
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLTDTAKQIKT 300
Db 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLTDTAKQIKT 370
Qy 301 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAMLGEL 360
Db 371 KVNKHAFFSGGRDITIEHRQFGGNCDDVVSFMYLTFFLEDDDKLEQIRKDYTSGAMLGEL 430
Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471

RESULT 13
US-10-370-715B-250
; Sequence 250, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: PI948R1-US
; CURRENT APPLICATION NUMBER: US/10/370, 715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 250
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-250

Query Match      100.0%; Score 2116; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVNP 120
Db 131 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVNP 190
Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFFSDLDYMGSSGFYKN 180
Db 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGFDINKTFFSDLDYMGSSGFYKN 250
Qy 181 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTDSCIGKISFPALQAAPSFNSFPQIFRDRDTIOCLIPCA 310
Qy 241 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLTDTAKQIKT 300
Db 311 IDQDPYFRMTRDVAPRIGYKPKALLHSTFFPALQGAQTKMSASDPNSISFLTDTAKQIKT 370

Query Match      100.0%; Score 2116; DB 16; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.9e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDTEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130
Qy 61 FLRGIFFSHRDMNQVLDAYENKPFYLYTGRGSSSEAMHVGLIPIFTKWLQDVNP 120
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Qy 301 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 360
Db 371 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 471

RESULT 14
US-09-813-718-10
; Sequence 10, Application US/09813718
; Publication No. US20020182666A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Kelsuke
; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
; FILE REFERENCE: 00-221
; CURRENT APPLICATION NUMBER: US/09/813,718
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human
; OTHER INFORMATION: full-length trpRS in pet20B
US-09-813-718-10
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Query Match 100.0%; Score 2116; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 5.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130

Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLDQVFNVP 120
Db 131 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLDQVFNVP 190

Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSSGFYKN 180
Db 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSSGFYKN 250

Qy 181 VVKIQKHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIIPRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIIPRDRDTIOCLIPCA 310

Qy 241 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQGAQTMSASDPNSSIFLDTAKOIKT 300
Db 311 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQGAQTMSASDPNSSIFLDTAKOIKT 370

Qy 301 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 360
Db 371 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 471
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RESULT 15
US-10-080-839-1
; Sequence 1, Application US/10080839
; Publication No. US20030017564A1
; GENERAL INFORMATION:
; APPLICANT: Schimmel, Paul
; APPLICANT: Wakasugi, Kelsuke
```

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; APPLICANT: Friedlander, Martin
; TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
; FILE REFERENCE: TSRI-813.1
; CURRENT APPLICATION NUMBER: US/10/080,839
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/270,951
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant human trpRS
US-10-080-839-1
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Query Match 100.0%; Score 2116; DB 14; Length 484;
Best Local Similarity 100.0%; Pred. No. 5.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 60
Db 71 SNHGPDATAEEDFVDPWTQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRP 130

Qy 61 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLDQVFNVP 120
Db 131 FLRRGIFFSHRDMNQVLDAVENKKPFYLYTGRGSSSEAMHVGHLPFIPTKWLDQVFNVP 190

Qy 121 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSSGFYKN 180
Db 191 LVQMTDDEKYLWKDLTLDOAYGDAVENAKDIIACGPDINKTIFSDLDYMGSSSGFYKN 250

Qy 181 VVKIQKHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIIPRDRDTIOCLIPCA 240
Db 251 VVKIQKHVTNQVKGIFGFTSDSCIGKISPPAIQAAPSFNSPQIIPRDRDTIOCLIPCA 310

Qy 241 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQGAQTMSASDPNSSIFLDTAKOIKT 300
Db 311 IDQDPYFRMTDVA PRIGYKPKALLHSTFFPALQGAQTMSASDPNSSIFLDTAKOIKT 370

Qy 301 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 360
Db 371 KVNKHAFCGGRTTIEHRQFGGNCVDVSPWYLTFFLEDDDKLEQIRKDYTSGLMTGEL 430

Qy 361 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 401
Db 431 KKALIEVLQPLIAEHQARRKEVTDEIVKEPMTPRKLSFDFQ 471
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Job time : 147 secs

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